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[54] HIV ENVELOPE POLYPEPTIDES

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[*] Notice: This patent is subject to a terminal disclaimer.

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Related U.S. Application Data

[60] Division of application No. 08/448,603, filed as application No. PCT/US94/06036, Jun. 7, 1994, Pat. No. 5,864,027, which is a continuation-in-part of application No. 08/072,833, Jun. 7, 1993, abandoned.

[51] Int. Cl.⁷ **A61K 39/21**; A61K 39/00;
A61K 39/38; A61K 39/12; C07K 1/00

[52] U.S. Cl. **424/208.1**; 424/184.1;
424/187.1; 424/188.1; 424/204.1; 424/207.1;
530/350; 536/23.1

[58] Field of Search 536/23.1; 424/184.1,
424/187.1, 188.1, 204.1, 207.1, 208.1; 530/350

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[57] ABSTRACT

A method for the rational design and preparation of vaccines based on HIV envelope polypeptides is described. In one embodiment, the method for making an HIV gp120 subunit vaccine for a geographic region comprises determining neutralizing epitopes in the V2 and/or C4 domains of gp120 of HIV isolates from the geographic region and selecting an HIV strain having gp120 a neutralizing epitope in the V2 or C4 domain which is common among isolates in the geographic region. In a preferred embodiment of the method, neutralizing epitopes for the V2, V3, and C4 domains of gp120 are determined. At least two HIV isolates having different neutralizing epitopes in the V2, V3, or C4 domain are selected and used to make the vaccine. The invention also provides a multivalent HIV gp120 subunit vaccine.

15 Claims, 10 Drawing Sheets

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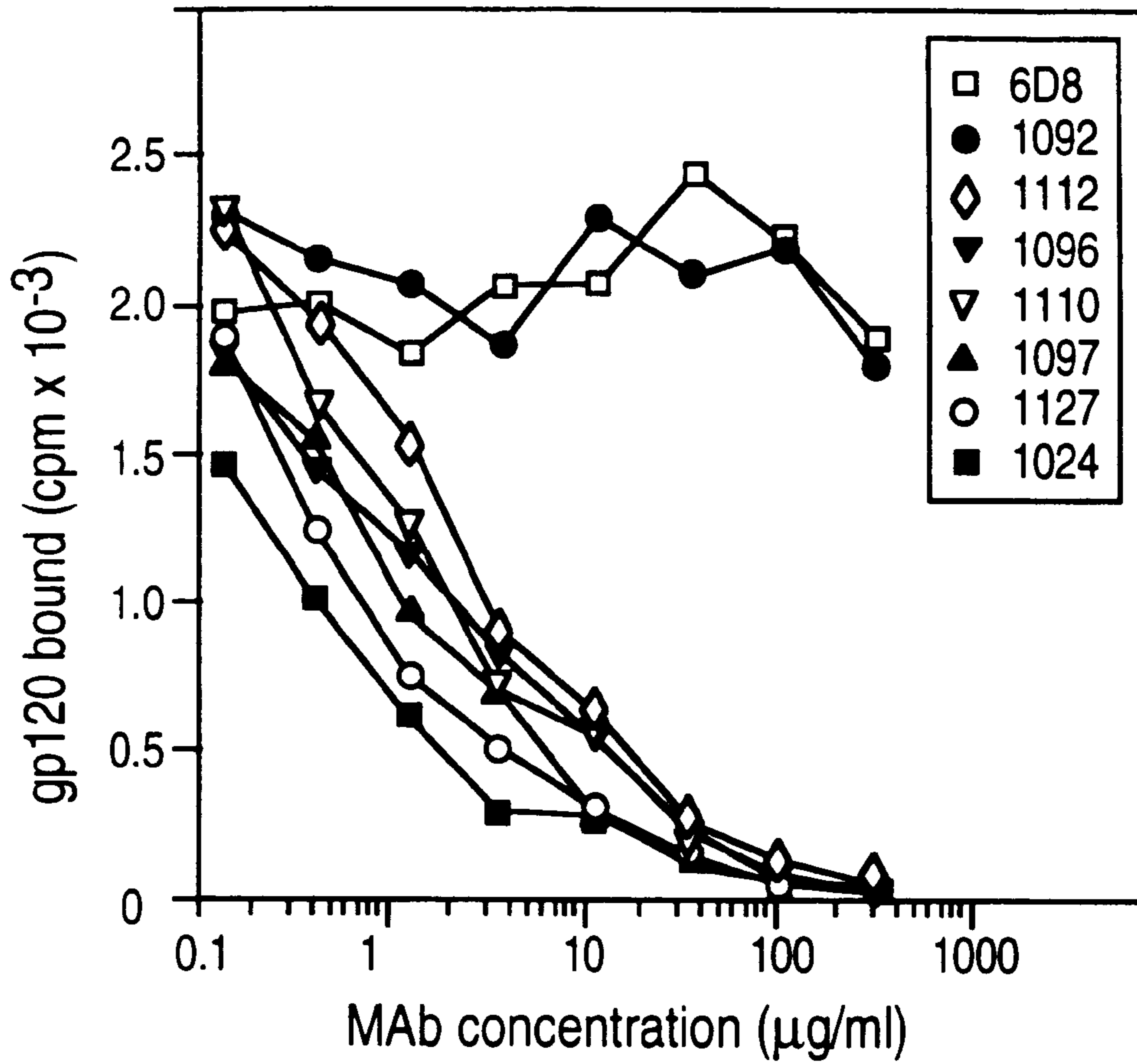


FIG. 1

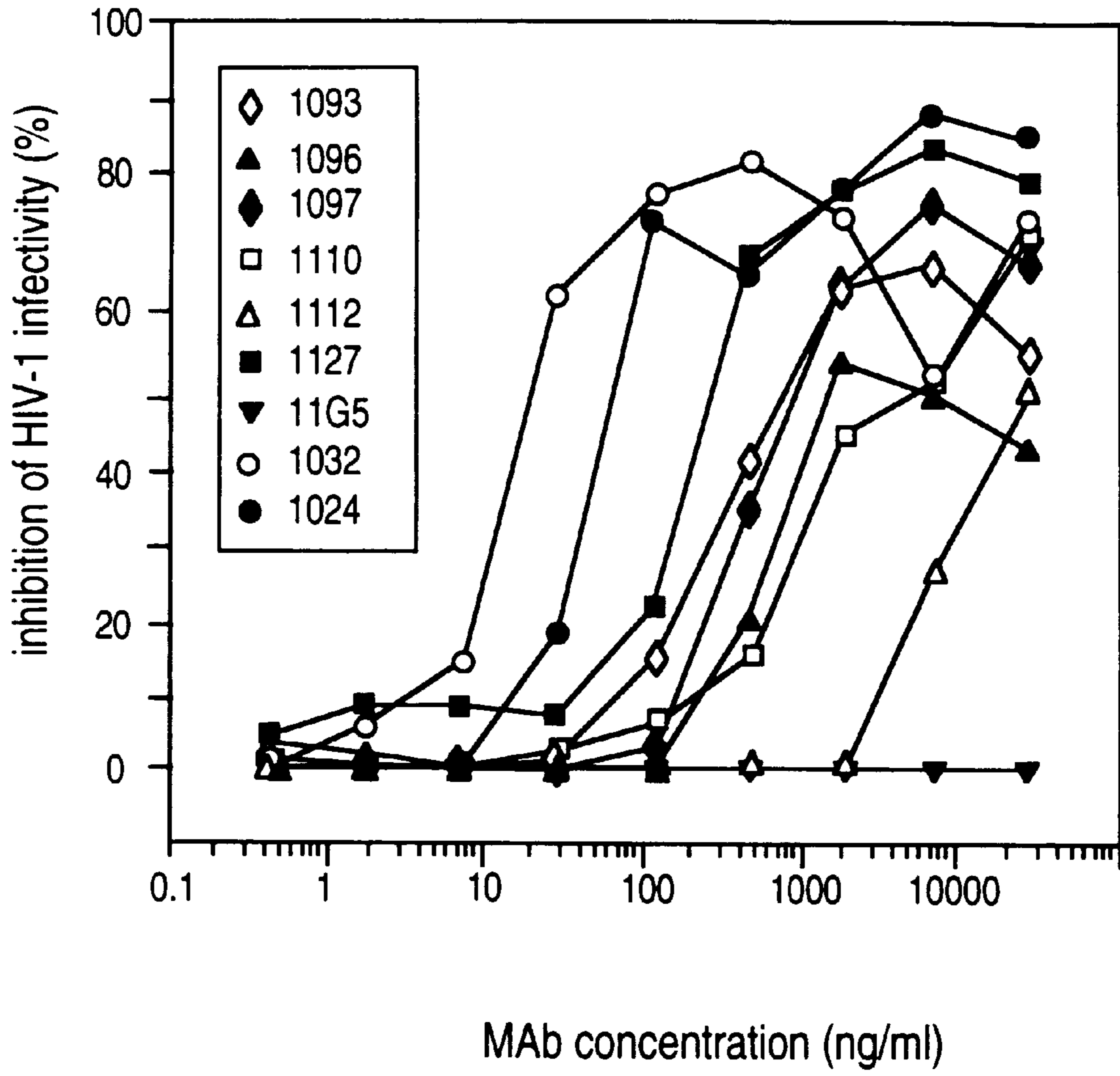


FIG. 2

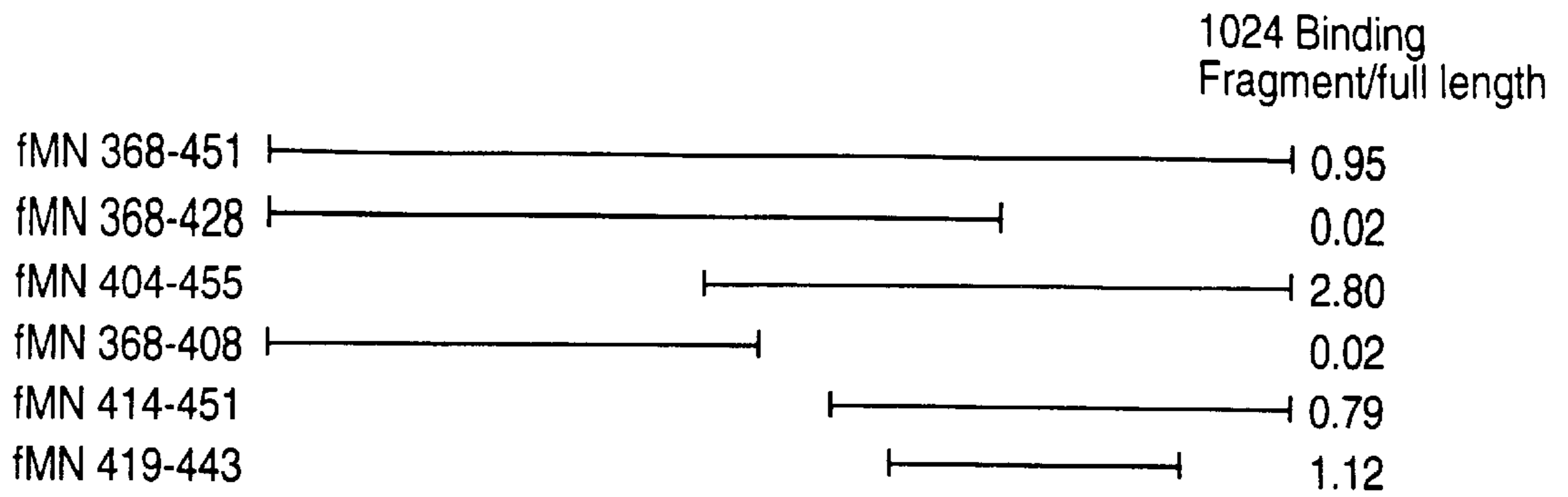


FIG. 3A

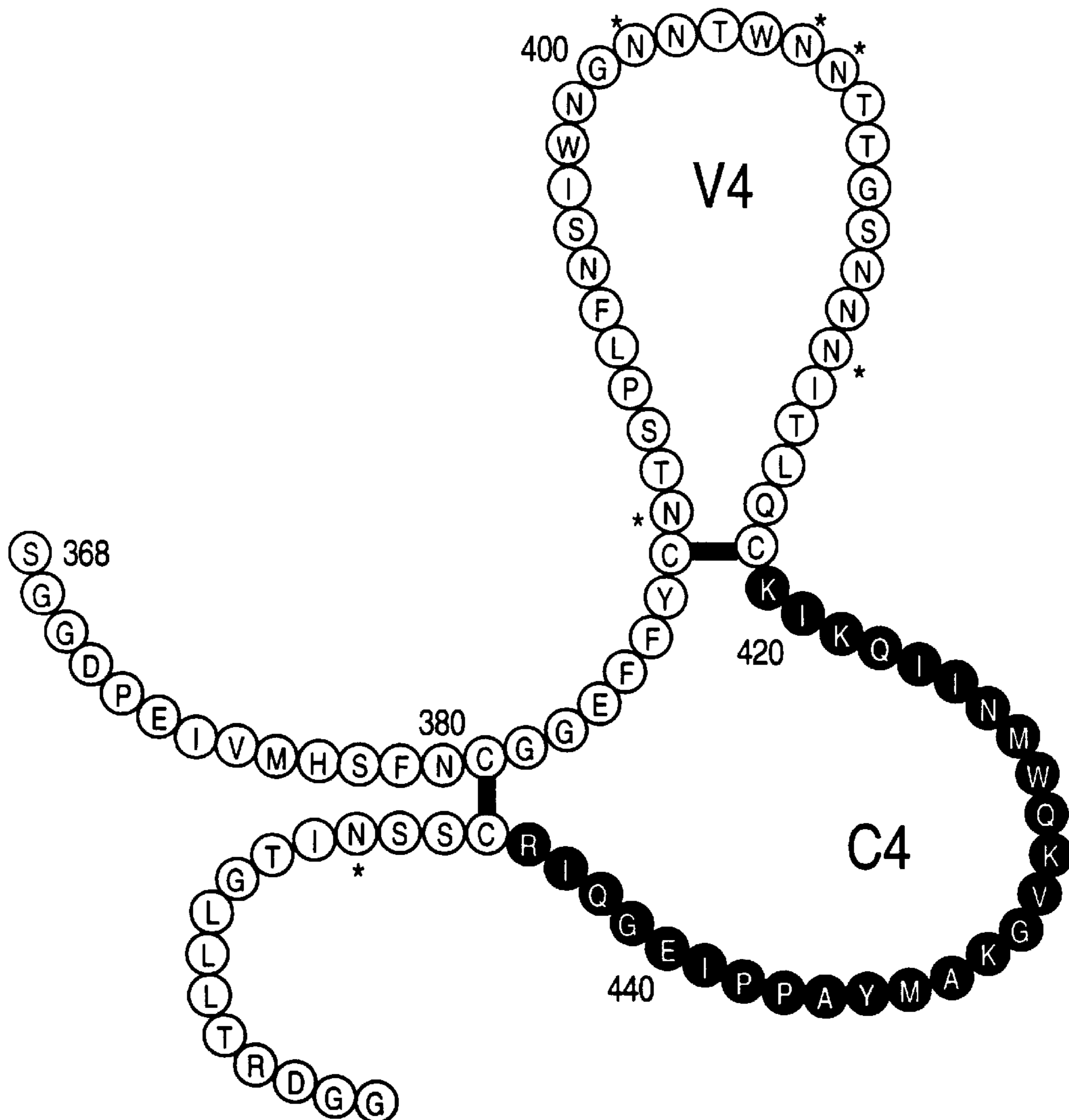


FIG. 3B

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418          445
CKIKQIINMWQKGKAMYAPPIEGQIRC  MNGNE (SEQ. ID. NO. 3)
-----E-----MN1984 (SEQ. ID. NO. 4)
-R-----E-----K-----JRCSF (SEQ. ID. NO. 5)
-R-----E-----N-----Z6 (SEQ. ID. NO. 6)
-R-----R--E--I--S-----NY5 (SEQ. ID. NO. 7)
-R-----V-----K-V-K-----Z321 (SEQ. ID. NO. 8)
-----GA-Q-----S-T-N-----A244 (SEQ. ID. NO. 9)

-R--F--E--S-----LAIIIIB', LAIBRU', LAIHXB3 (SEQ. ID. NO. 10)
-----I--K-----S-----LAIHXB2 (SEQ. ID. NO. 11)
-R--I--E--S-----LAIBH10' LAIHXB3 (SEQ. ID. NO. 12)
-----E-----MN1984 (SEQ. ID. NO. 13)

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FIG. 4

418	445		
CKIKQIINMWQKVGKAMYAPPIEGQIRC		MNGNE	(SEQ. ID. NO. 3)
-----E-----		MN. 429E	(SEQ. ID. NO. 15)
-----A-----		MN. 429A	(SEQ. ID. NO. 16)
-A-----		MN. 419A	(SEQ. ID. NO. 17)
-----A-----		MN. 421A	(SEQ. ID. NO. 18)
-----A-----		MN. 432A	(SEQ. ID. NO. 19)
-----A-----		MN. 440A	(SEQ. ID. NO. 20)
-R--F--E--S--		LAI IIB	(SEQ. ID. NO. 21)
-----F-----		MN. 423F	(SEQ. ID. NO. 22)
-----F--E-----		MN. 423F, 429E	(SEQ. ID. NO. 23)

FIG. 5

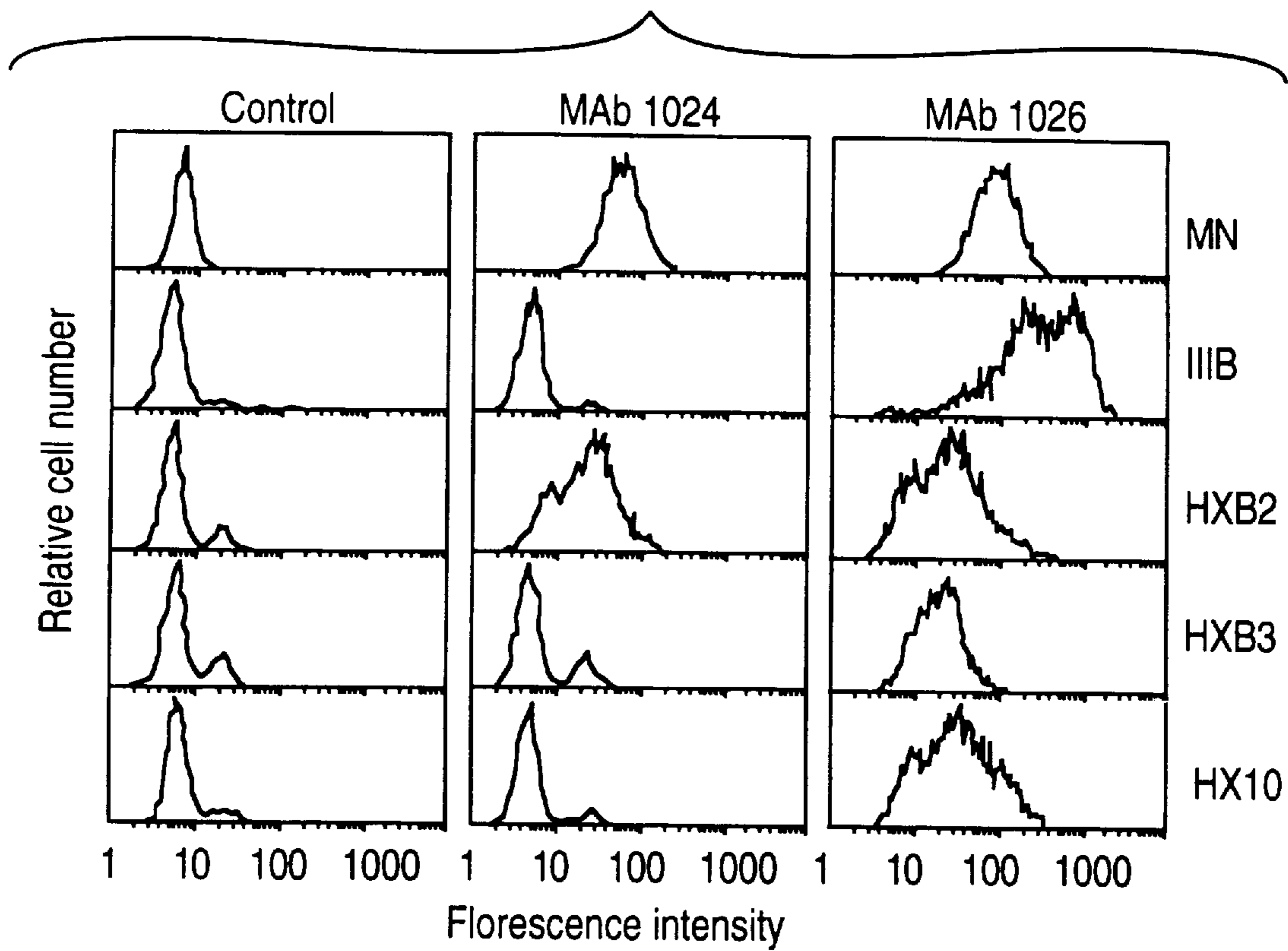


FIG. 6

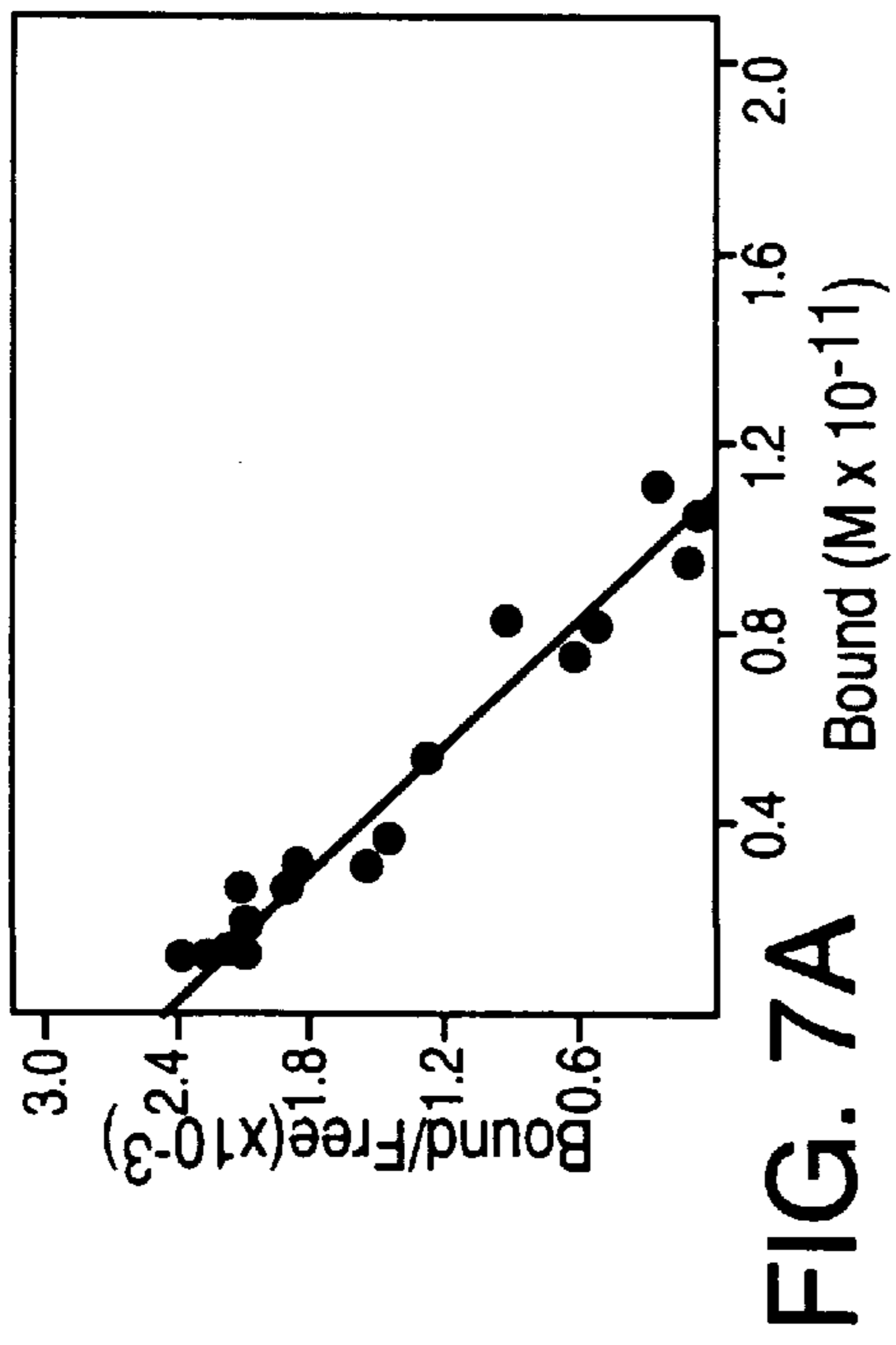


FIG. 7A

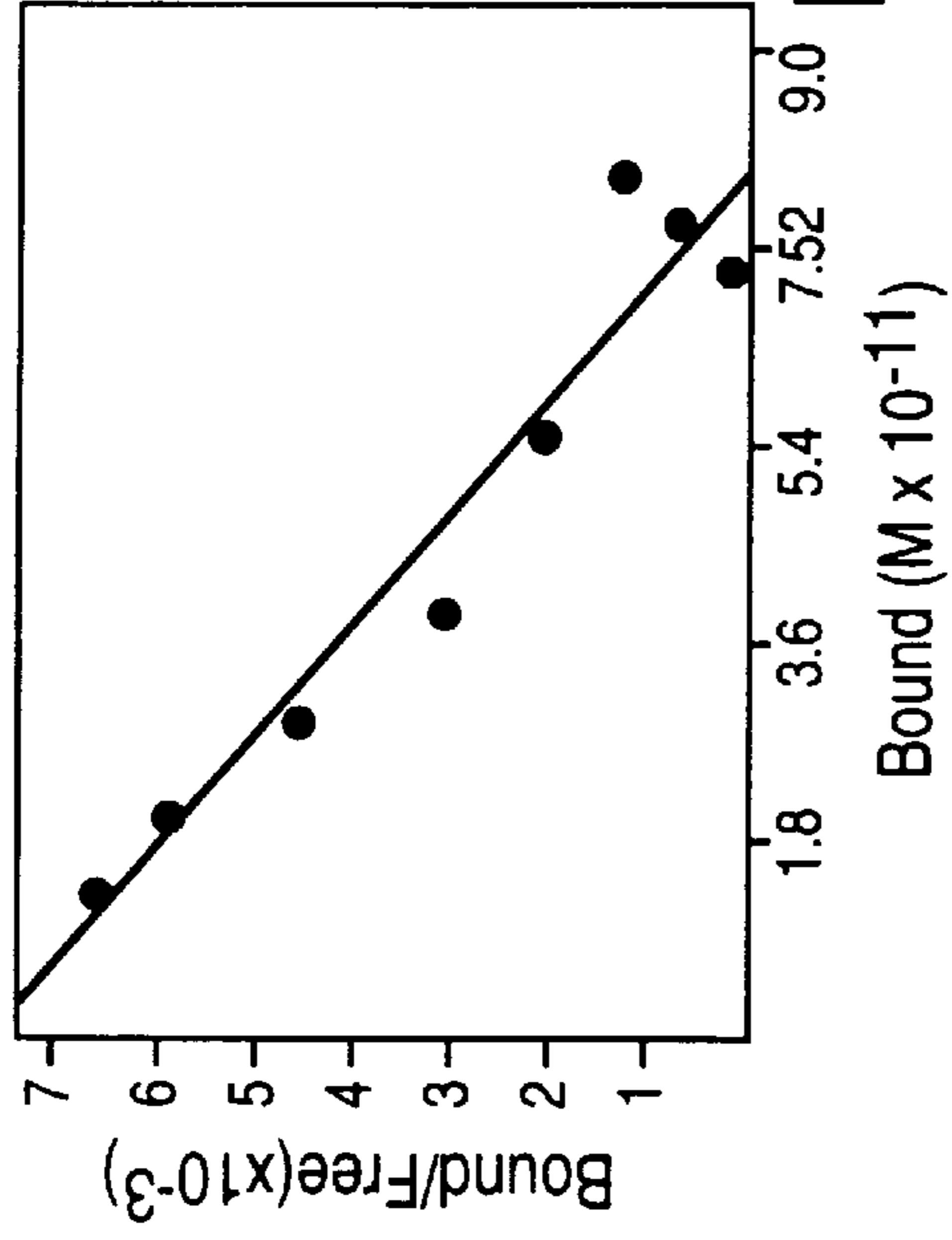


FIG. 7B

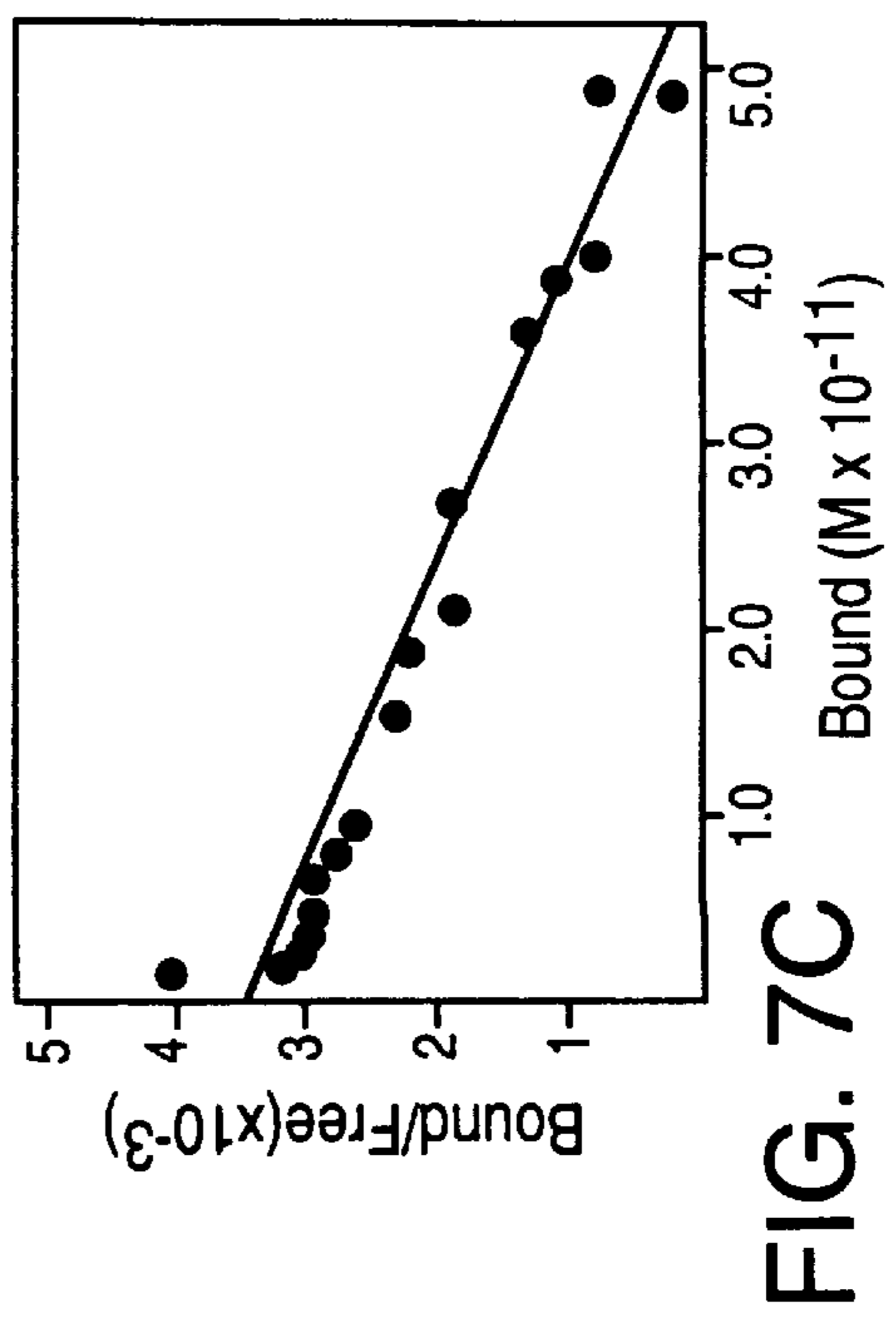


FIG. 7C

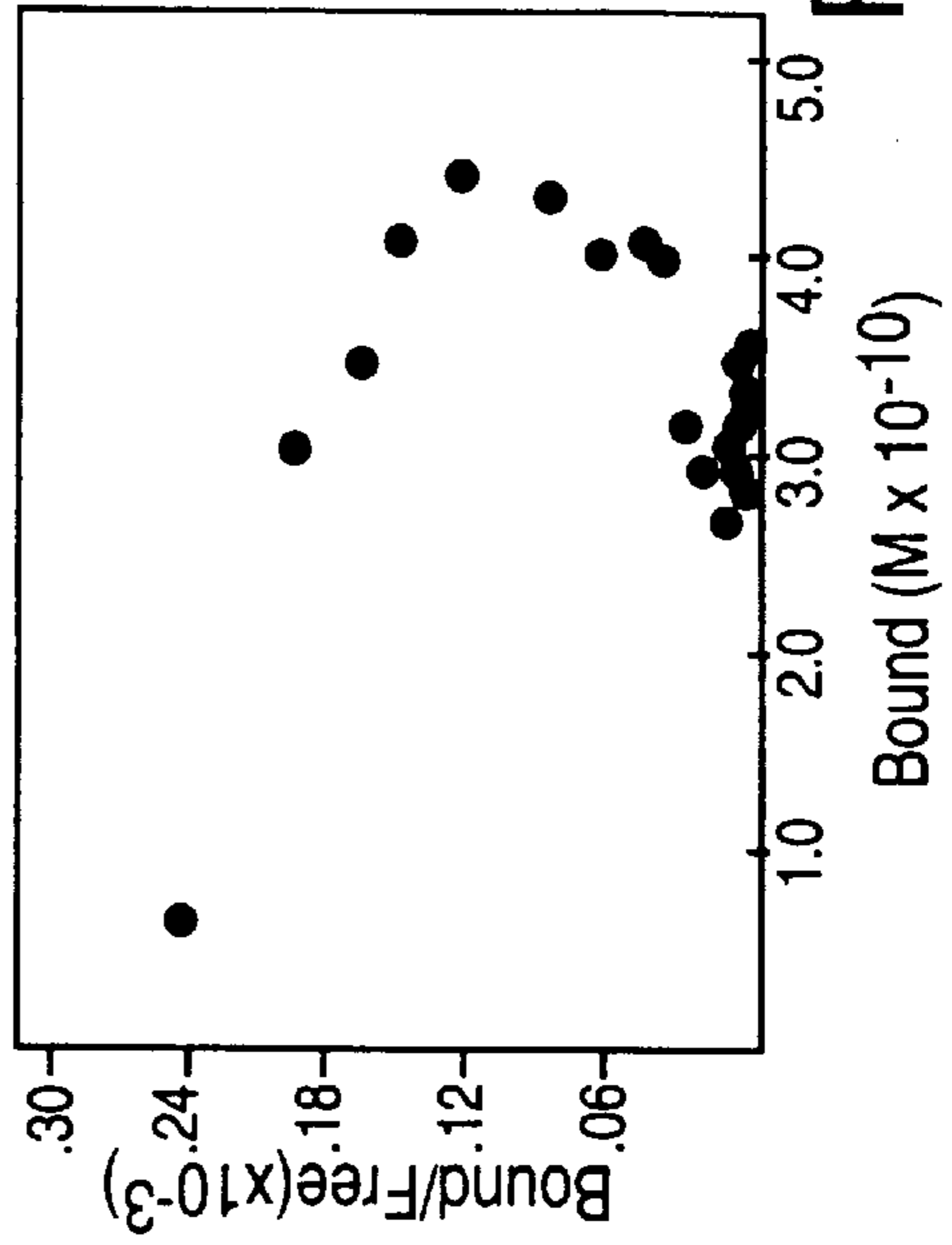


FIG. 7D

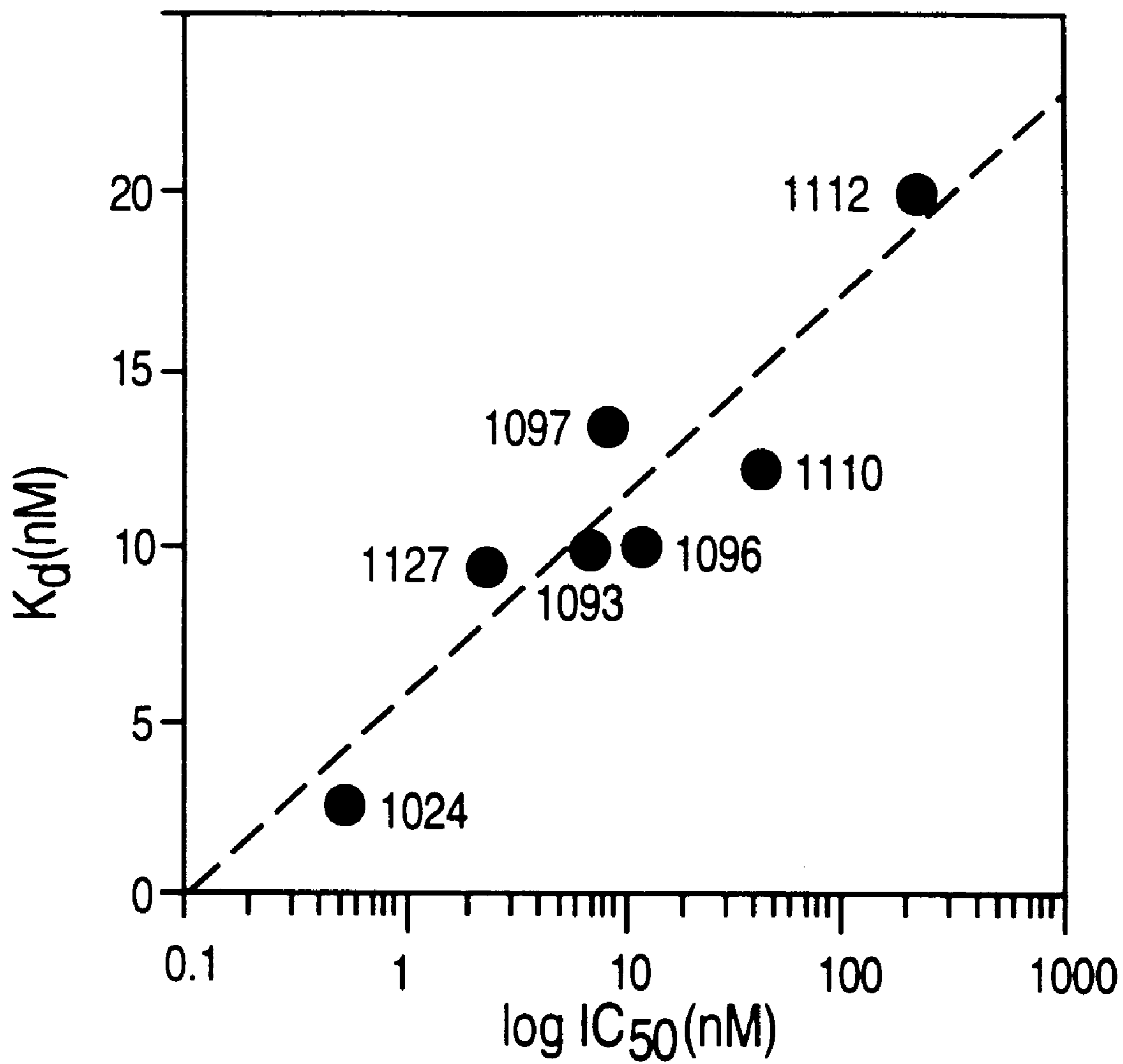


FIG. 8

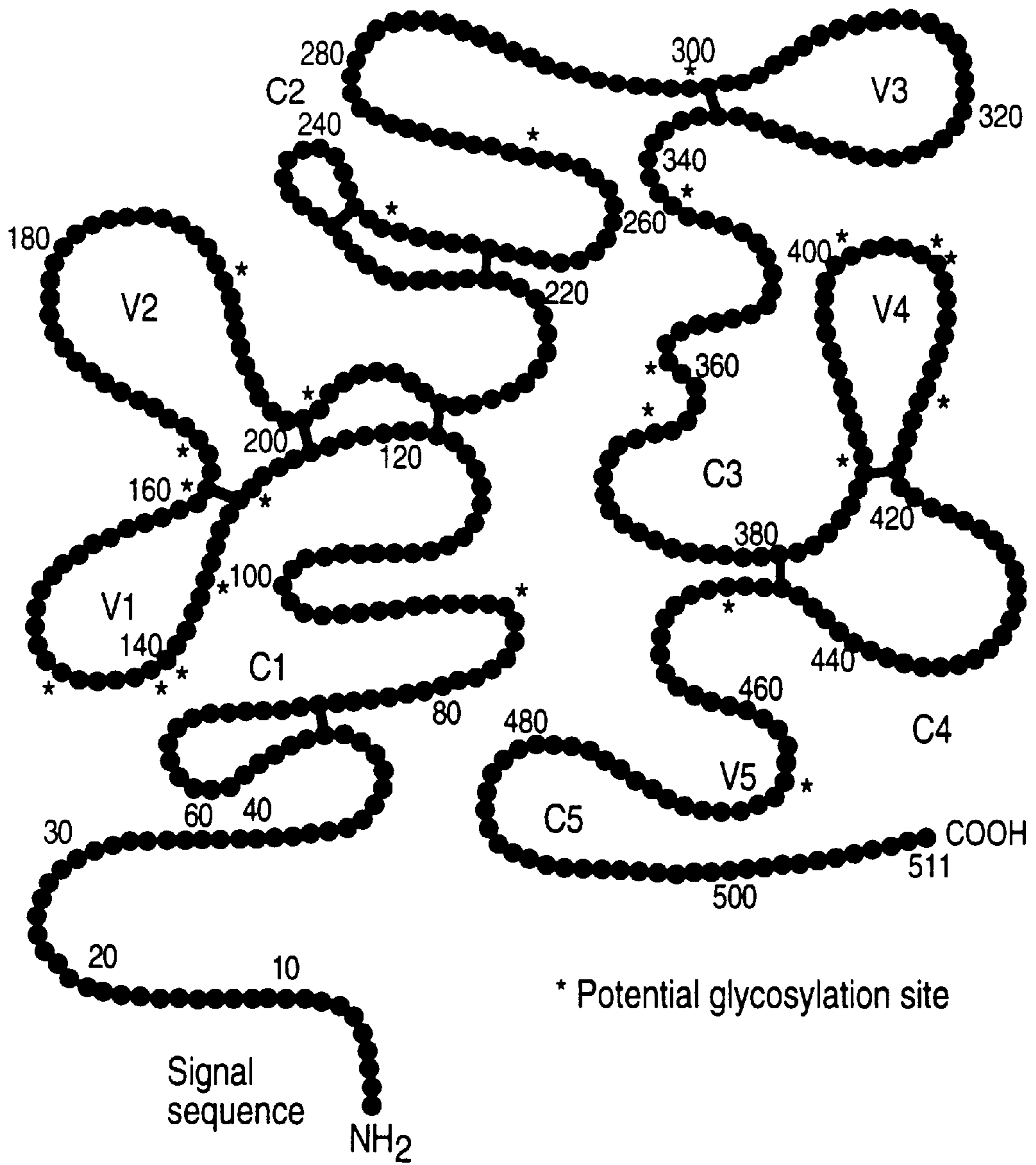


FIG. 9

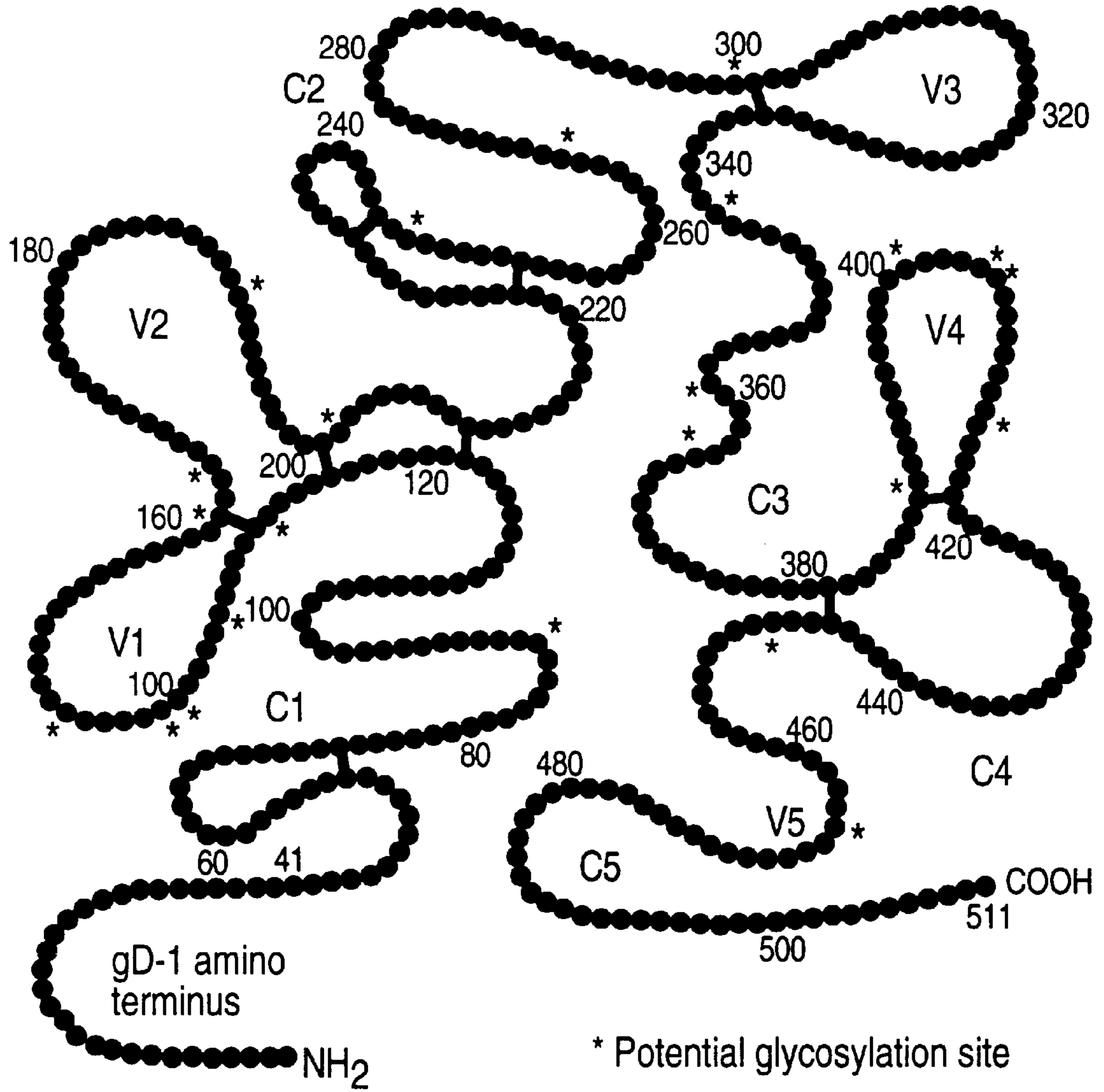


FIG. 10

HIV ENVELOPE POLYPEPTIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a divisional of application Ser. No. 08/448,603, filed Oct. 10, 1998, now U.S. Pat. No. 5,864,027, which is a 35 U.S.C. 371 of PCT/US94/06036, filed Jun. 7, 1994, which is a continuation-in-part of application Ser. No. 08/072,833, filed Jun. 7, 1993, now abandoned.

FIELD OF THE INVENTION

This invention relates to the rational design and preparation of HIV vaccines based on HIV envelope polypeptides and the resultant vaccines. This invention further relates to improved methods for HIV serotyping and immunogens which induce antibodies useful in the serotyping methods.

BACKGROUND OF THE INVENTION

Acquired immunodeficiency syndrome (AIDS) is caused by a retrovirus identified as the human immunodeficiency virus (HIV). There has been intense effort to develop a vaccine. These efforts have focused on inducing antibodies to the HIV envelope protein. Recent efforts have used subunit vaccines where an HIV protein, rather than attenuated or killed virus, is used as the immunogen in the vaccine for safety reasons. Subunit vaccines generally include gp120, the portion of the HIV envelope protein which is on the surface of the virus.

The HIV envelope protein has been extensively described, and the amino acid and RNA sequences encoding HIV envelope from a number of HIV strains are known (Myers, G. et al., 1992. *Human Retroviruses and AIDS*. A compilation and analysis of nucleic acid and amino acid sequences. Los Alamos National Laboratory, Los Alamos, N. Mex.). The HIV envelope protein is a glycoprotein of about 160 kd (gp160) which is anchored in the membrane bilayer at its carboxyl terminal region. The N-terminal segment, gp120, protrudes into the aqueous environment surrounding the virion and the C-terminal segment, gp41, spans the membrane. Via a host-cell mediated process, gp160 is cleaved to form gp120 and the integral membrane protein gp41. As there is no covalent attachment between gp120 and gp41, free gp120 is released from the surface of virions and infected cells.

The gp120 molecule consists of a polypeptide core of 60,000 daltons which is extensively modified by N-linked glycosylation to increase the apparent molecular weight of the molecule to 120,000 daltons. The amino acid sequence of gp120 contains five relatively conserved domains interspersed with five hypervariable domains. The positions of the 18 cysteine residues in the gp120 primary sequence, and the positions of 13 of the approximately 24 N-linked glycosylation sites in the gp120 sequence are common to all gp120 sequences. The hypervariable domains contain extensive amino acid substitutions, insertions and deletions. Sequence variations in these domains result in up to 30% overall sequence variability between gp120 molecules from the various viral isolates. Despite this variation, all gp120 sequences preserve the virus's ability to bind to the viral receptor CD4 and to interact with gp41 to induce fusion of the viral and host cell membranes.

Gp120 has been the object of intensive investigation as a vaccine candidate for subunit vaccines, as the viral protein which is most likely to be accessible to immune attack. Gp120 is considered to be a good candidate for a subunit

vaccine, because (i) gp120 is known to possess the CD4 binding domain by which HIV attaches to its target cells, (ii) HIV infectivity can be neutralized in vitro by antibodies to gp 120, (iii) the majority of the in vitro neutralizing activity present in the serum of HIV infected individuals can be removed with a gp120 affinity column, and (iv) the gp120/gp41 complex appears to be essential for the transmission of HIV by cell-to-cell fusion.

The identification of epitopes recognized by virus neutralizing antibodies is critical for the rational design of vaccines effective against HIV-1 infection. One way in which antibodies would be expected to neutralize HIV-1 infection is by blocking the binding of the HIV-1 envelope glycoprotein, gp120, to its cellular receptor, CD4. However, it has been surprising that the CD4 blocking activity, readily demonstrated in sera from HIV-1 infected individuals (31, 44) and animals immunized with recombinant envelope glycoproteins (1-3), has not always correlated with neutralizing activity (2, 31, 44). Results obtained with monoclonal antibodies have shown that while some of the monoclonal antibodies that block the binding of gp120 to CD4 possess neutralizing activity, others do not (4, 7, 16, 26, 33, 35, 43, 45). When the neutralizing activity of CD4 blocking monoclonal antibodies are compared to those directed to the principal neutralizing determinant (PND) located in the third variable domain (V3 domain) of gp120 (10, 39), the CD4 blocking antibodies appear to be significantly less potent. Thus, CD4 blocking monoclonal antibodies typically exhibit 50% inhibitory concentration values (IC_{50}) in the 1-10 $\mu\text{g/ml}$ range (4, 16, 26, 33, 35, 43, 45) whereas PND directed monoclonal antibodies typically exhibit IC_{50} values in the 0.1 to 1.0 $\mu\text{g/ml}$ range (23, 33, 42).

Subunit vaccines, based on gp120 or another viral protein, that can effectively induce antibodies that neutralize HIV are still being sought. However, to date no vaccine has not been effective in conferring protection against HIV infection.

DESCRIPTION OF THE BACKGROUND ART

Recombinant subunit vaccines are described in Berman et al., PCT/US91/02250 (published as number WO91/15238 on Oct. 17, 1991). See also, e.g. Hu et al., *Nature* 328:721-724 (1987) (vaccinia virus-HIV envelope recombinant vaccine); Arthur et al., *J. Virol.* 63(12): 5046-5053 (1989) (purified gp120); and Berman et al., *Proc. Natl. Acad. Sci. USA* 85:5200-5204 (1988) (recombinant envelope glycoprotein gp120).

Numerous sequences for gp120 are known. The sequence of gp120 from the IIIB substrain of HIV-1_{LAI} referred to herein is that determined by Muesing et al., "Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus, *Nature* 313:450-458 (1985). The sequences of gp120 from the NY-5, Jrcsf, Z6, Z321, and HXB2 strains of HIV-1 are listed by Myers et al., "Human Retroviruses and AIDS; A compilation and analysis of nucleic acid and amino acid sequences," Los Alamos National Laboratory, Los Alamos, N. Mex. (1992). The sequence of the Thai isolate A244 is provided by McCutchan et al., "Genetic Variants of HIV-1 in Thailand," *AIDS Res. and Human Retroviruses* 8:1887-1895 (1992). The MN₁₉₈₄ clone is described by Gurgo et al., "Envelope sequences of two new United States HIV-1 isolates," *Virol.* 164: 531-536 (1988). The amino acid sequence of this MN clone differs by approximately 2% from the MN-gp120 clone (MN_{GNE}) disclosed herein and obtained by Berman et al.

Each of the above-described references is incorporated herein by reference in its entirety.

SUMMARY OF THE INVENTION

The present invention provides a method for the rational design and preparation of vaccines based on HIV envelope polypeptides. This invention is based on the discovery that there are neutralizing epitopes in the V2 and C4 domains of gp120, in addition to the neutralizing epitopes in the V3 domain. In addition, the amount of variation of the neutralizing epitopes is highly constrained, facilitating the design of an HIV subunit vaccine that can induce antibodies that neutralize a plurality of HIV strains for a given geographic region.

In one embodiment, the present invention provides a method for making an HIV gp120 subunit vaccine for a geographic region in which a neutralizing epitope in the V2 and/or C4 domains of gp120 of HIV isolates from the geographic region is determined and an HIV strain having gp120 which has a neutralizing epitope in the V2 or C4 domain which is common among isolates in the geographic region is selected and used to make the vaccine.

In a preferred embodiment of the method, neutralizing epitopes for the V2, V3, and C4 domains of gp120 from HIV isolates from the geographic region are determined. At least two HIV isolates having different neutralizing epitopes in the V2, V3, or C4 domain are selected and used to make the HIV gp120 subunit vaccine. Preferably, each of the selected isolates have one of the most common neutralizing epitopes for the V2, V3, or C4 domains.

The invention also provides a multivalent HIV gp120 subunit vaccine. The vaccine comprises gp120 from two isolates of HIV having at least one different neutralizing epitope. Preferably, the isolates have the most common neutralizing epitopes in the geographic region for one of the domains.

A DNA sequence of less than 5 kilobases encoding gp120 from preferred vaccine strains of HIV, GNE₈ and GNE₁₆, expression construct comprising the GNE₈-gp120 and GNE₁₆-gp120 encoding DNA under the transcriptional and translational control of a heterologous promoter, and isolated GNE₈-gp120 and GNE₁₆-gp120 are also provided. The invention further provides improved methods for HIV serotyping in which epitopes in the V2 or C4 domains of gp120 are determined and provides immunogens (truncated gp120 sequences) which induce antibodies useful in the serotyping methods.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 describes inhibition of CD4 binding by monoclonal antibodies to recombinantly produced gp120 from the MN strain of HIV (MN-rgp120). Mice were immunized with MN-rgp120 and the resulting splenocytes were fused with the NP3X63.Ag8.653 cell line as described in Example 1. Thirty-five stable hybridoma clones, reactive with MN-rgp120 were identified by ELISA. Secondary screening revealed seven cell lines (1024, 1093, 1096, 1097, 1110, 1112, and 1027) secreting antibodies able to inhibit the binding of MN-rgp120 to biotin labeled recombinantly produced CD4 (rsCD4) in a ELISA using HRP-streptavidin. Data obtained with monoclonal antibodies from the same fusion (1026, 1092, 1126) that failed to inhibit MN-rgp120 binding to CD4 is shown for purposes of comparison.

FIG. 2 shows neutralizing activity of CD4-blocking monoclonal antibodies to MN-rgp120. Monoclonal antibodies that blocked the binding of MN-rgp120 to CD4 were screened for the capacity to inhibit the infection of MT2

cells by the MN strain of HIV-1 in vitro. Cell free virus was added to wells containing serially diluted antibodies and incubated at 4° C. for 1 hr. After incubation, MT-2 cells were added to the wells and the cultures were then grown for 5 days at 37° C. Cell viability was then measured by addition of the colorimetric tetrazolium compound MTT as described in reference (35) of Example 1. The optical densities of each well were measured at 540 nm using a microtiter plate reading spectrophotometer. Inhibition of virus infectivity was calculated by dividing the mean optical densities from wells containing monoclonal antibodies by the mean value of wells that received virus alone. Monoclonal antibodies that blocked CD4 binding are the same as those indicated in Figure Legend 1. Data from the V3-directed monoclonal antibody to MN-rgp120 (1034) is provided as a positive control. Data obtained with the V3 directed monoclonal antibody, 11G5, specific for the IIIB strain of HIV-1 (33) is shown as a negative control.

FIGS. 3A-3B are a diagram of gp120 fragments used to localize the epitopes recognized by the CD4 blocking monoclonal antibodies to MN-rgp120. A series of fragments (A) corresponding to the V4 and C4 domains (B) (SEQ. ID. NO. 14) of the gene encoding MN-rgp120 were prepared by PCR. The gp120 gene fragments were fused to a fragment of the gene encoding Herpes Simplex Virus Type 1 glycoprotein D that encoded the signal sequence and 25 amino acids from the mature amino terminus. The chimeric genes were assembled into a mammalian cell expression vector (PRK5) that provided a CMV promoter, translational stop codons and an SV40 polyadenylation site. The embryonic human kidney adenocarcinoma cell line, 293s, was transfected with the resulting plasmid and recombinant proteins were recovered from growth conditioned cell culture medium.

Fragments of MN-rgp120, expressed as HSV-1 Gd fusion proteins, were produced by transient transfection of 293s cells (Example 1). To verify expression, cells were metabolically labeled with [³⁵S]-methionine, and the resulting growth conditioned cell culture supernatants were immunoprecipitated (c) using a monoclonal antibody, 5B6, specific for the amino terminus of HSV-1 Gd and fixed *S. aureus*. The immunoprecipitated proteins were resolved on 4 to 20% acrylamide gradient gels using SDS-PAGE and visualized by autoradiography. The samples were: Lane 1, FMN.368-408; lane 2, FMN.368-451; lane 3, FMN.419-443; lane 4, FMN.414-451; lane 5, MN-rgp120. The gel demonstrated that the proteins were expressed and migrated at the expected molecular weights.

FIG. 4 shows a C4 domain sequence comparison (SEQ. ID. Nos. 3-13). The C4 domain amino acid sequences of recombinant and virus derived gp120s used for monoclonal antibody binding studies were aligned starting the amino terminal cysteine. Amino acid positions are designated with respect to the sequence of MN-rgp120. Sequences of the LAI substrains, IIIB, BH10, Bru, HXB2, and HXB3 are shown for purposes of comparison.

FIG. 5 shows sequences of C4 domain mutants of MN-rgp120 (SEQ. ID. Nos. 3 and 15-23). Nucleotide substitutions, resulting in the amino acid sequences indicated, were introduced into the C4 domain of MN-rgp120 gene using recombinant PCR. The resulting variants were assembled into the expression plasmid, pRK5, which was then transfected into 293s cells. The binding of monoclonal antibodies to the resulting C4 domain variants was then analyzed (Table 5) by ELISA.

FIG. 6 illustrates the reactivity of monoclonal antibody 1024 with HIV-1_{LAI} substrains. The cell surface binding of

the C4 domain reactive monoclonal antibody 1024 to H9 cells chronically infected with the IIB, HXB2, HXB3, and HXB10 substrains of HIV-1 LAI or HIV-1MN was analyzed by flow cytometry. Cultures of virus infected cells were reacted with either monoclonal antibody 1024, a nonrelevant monoclonal antibody (control), or a broadly cross reactive monoclonal antibody (1026) raised against rgp120. After washing away unbound monoclonal antibody, the cells were then labeled with fluorescein conjugated goat antibody to mouse IgG (Fab')₂, washed and fixed with paraformaldehyde. The resulting cells were analyzed for degree of fluorescence intensity using a FACSCAN (Becton Dickenson, Fullerton, Calif.). Fluorescence was measured as mean intensity of the cells expressed as mean channel number plotted on a log scale.

FIGS. 7A-7D show the determination of the binding affinity of monoclonal antibodies for MN-rgp120. CD4 blocking monoclonal antibodies raised against MN-rgp120 (1024 and 1097) or IIB-rgp120 (13H8 and 5C2) were labeled with [¹²⁵I] and binding titrations using MN-rgp120 (A and B) or IIB-rgp120 (C and D) were carried out as described in the Example 1. A, binding of monoclonal antibody 1024; B binding of monoclonal antibody 1097; C, binding of monoclonal antibody 13H8; and D binding of monoclonal antibody 5C2.

FIG. 8 shows the correlation between gp120 binding affinity (K_d) and neutralizing activity (IC₅₀) of monoclonal antibodies to the C4 domain of MN-rgp120. Binding affinities of monoclonal antibodies to the C4 domain of gp120 were determined by Scatchard analysis (FIG. 9, Table 5). The resulting values were plotted as a function of the log of their neutralizing activities (IC₅₀) determined in FIG. 2 and Table 6.

FIG. 9 depicts the amino acid sequence of the mature envelope glycoprotein (gp120) from the MN_{GENE} clone of the MN strain of HIV-1 (SEQ. ID. NO. 1). Hypervariable domains are from 1-29 (signal sequence), 131-156, 166-200, 305-332, 399-413, and 460-469. The V and C regions are indicated (according to Modrow et al., *J. Virology* 61(2):570 (1987)). Potential glycosylation sites are marked with a (*).

FIG. 10 depicts the amino acid sequence of a fusion protein of the residues 41-511 of the mature envelope glycoprotein (gp120) from the MN_{GENE} clone of the MN strain of HIV-1, and the gD-1 amino terminus from the herpes simplex glycoprotein gD-1. (SEQ. ID. NO. 2). The V and C regions are indicated (according to Modrow et al., *J. Virology* 61(2):570 (1987)). Potential glycosylation sites are marked with a (*).

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a method for the rational design and preparation of vaccines based on HIV envelope polypeptides. This invention is based on the discovery that there are neutralizing epitopes in the V2 and C4 domains of gp120, in addition to the neutralizing epitopes in the V3 domain. Although the amino acid sequences of the neutralizing epitopes in the V2, V3, and C4 domains are variable, it has now been found that the amount of variation is highly constrained. The limited amount of variation facilitates the design of an HIV subunit vaccine that can induce antibodies that neutralize the most common HIV strains for a given geographic region. In particular, the amino acid sequence of neutralizing epitopes in the V2, V3, and C4 domains for isolates of a selected geographic region is determined.

gp120 from isolates having the most common neutralizing epitope sequences are utilized in the vaccine.

The invention also provides a multivalent gp120 subunit vaccine wherein gp120 present in the vaccine is from at least two HIV isolates which have different amino acid sequences for a neutralizing epitope in the V2, V3, or C4 domain of gp120. The invention further provides improved methods for HIV serotyping in which epitopes in the V2 or C4 domains of gp120 are determined and provides immunogens which induce antibodies useful in the serotyping methods.

The term "subunit vaccine" is used herein, as in the art, to refer to a viral vaccine that does not contain virus, but rather contains one or more viral proteins or fragments of viral proteins. As used herein, the term "multivalent" means that the vaccine contains gp120 from at least two HIV isolates having different amino acid sequences for a neutralizing epitope.

Vaccine Design Method

The vaccine design method of this invention is based on the discovery that there are neutralizing epitopes in the V2 and C4 domains of gp120, in addition to those found in the principal neutralizing domain (PND) in the V3 domain. Selecting an HIV isolate with appropriate neutralizing epitopes in the V2 and/or C4 domains provides a vaccine that is designed to induce immunity to the HIV isolates present in a selected geographic region. In addition, although the amino acid sequence of the V2, V3, and C4 domains containing the neutralizing epitopes is variable, the amount of variation is highly constrained, facilitating the design of a multivalent vaccine which can neutralize a plurality of the most common HIV strains for a given geographic region.

The method for making an HIV gp120 subunit vaccine depends on the use of appropriate strains of HIV for a selected geographic region. Appropriate strains of HIV for the region are selected by determining the neutralizing epitopes for HIV isolates and the percentage of HIV infections attributable to each strain present in the region. HIV strains which have the most common neutralizing epitopes in the V2 or C4 domains in the geographic region are selected. Preferably, isolates that confer protection against the most common neutralizing epitopes in the V2, V3, and C4 domains for a geographic region are selected.

One embodiment of the method for making an HIV gp120 subunit vaccine from appropriate strains of HIV for a geographic region comprises the following steps. A neutralizing epitope in the V2 or C4 domain of gp120 of HIV isolates from the geographic region is determined. An HIV strain having gp120 with a neutralizing epitope in the V2 or C4 domain that is common among HIV isolates in the geographic region is selected. gp120 from the selected isolate is used to make an HIV gp120 subunit vaccine.

In another embodiment of the method, the neutralizing epitopes in the V2, V3, and C4 domains of gp120 from HIV isolates from the geographic region are determined. At least two HIV isolates having different neutralizing epitopes in the V2, V3, or C4 domain are selected and used to make an HIV gp120 subunit vaccine. Preferably, the vaccine contains gp120 from at least the two or three HIV strains having the most common neutralizing epitopes for the V2, V3, or C4 domains. More preferably, the vaccine contains gp120 from sufficient strains so that at least about 50%, preferably about 70%, more preferably about 80% or more of the neutralizing epitopes for the V2, V3, and C4 domains in the geographic region are included in the vaccine. The location of the neutralizing epitopes in the V3 region are well known. The location of the neutralizing epitopes in the V2 and C4 regions are described hereinafter.

Each of the steps of the method are described in detail below.

Determining Neutralizing Epitopes

The first step in designing a vaccine for a selected geographic region is to determine the neutralizing epitopes in the gp120 V2 and/or C4 domains. In a preferred embodiment, neutralizing epitopes in the V3 domain (the principal neutralizing domain) are also determined. The location of neutralizing epitopes in the V3 domain is well known. Neutralizing epitopes in the V2 and C4 domains have now been found to be located between about residues 163 and 200 and between about residues 420 and 440, respectively. In addition, the critical residues for antibody binding are residues 171, 173, 174, 177, 181, 183, 187, and 188 in the V2 domain and residues 429 and 432 in the C4 domain, as described in detail in the Examples.

The neutralizing epitopes for any isolate can be determined by sequencing the region of gp120 containing the neutralizing epitope. Alternatively, when antibodies specific for the neutralizing epitope, preferably monoclonal antibodies, are available the neutralizing epitope can be determined by serological methods as described hereinafter. A method for identification of additional neutralizing epitopes in gp120 is described hereinafter.

When discussing the amino acid sequences of various isolates and strains of HIV, the most common numbering system refers to the location of amino acids within the gp120 protein using the initiator methionine residue as position 1. The amino acid numbering reflects the mature HIV-1 gp120 amino acid sequence as shown by FIGS. 9 and FIG. 10 [SEQ. ID Nos. 1 and 2]. For gp120 sequences derived from other HIV isolates and which include their native HIV N-terminal signal sequence, numbering may differ. Although the nucleotide and amino acid residue numbers may not be applicable in other strains where upstream deletions or insertions change the length of the viral genome and gp120, the region encoding the portions of gp120 is readily identified by reference to the teachings herein. The variable (V) domains and conserved (C) domains of gp120 are specified according to the nomenclature of Modrow et al. "Computer-assisted analysis of envelope protein sequences of seven human immunodeficiency virus isolates: predictions of antigenic epitopes in conserved and variable regions," *J. Virol.* 61:570-578 (1987).

The first step in identifying the neutralizing epitopes for any region of gp120 is to immunize an animal with gp120 to induce anti-gp120 antibodies. The antibodies can be polyclonal or, preferably, monoclonal. Polyclonal antibodies can be induced by administering to the host animal an immunogenic composition comprising gp120. Preparation of immunogenic compositions of a protein may vary depending on the host animal and the protein and is well known. For example, gp120 or an antigenic portion thereof can be conjugated to an immunogenic substance such as KLH or BSA or provided in an adjuvant or the like. The induced antibodies can be tested to determine whether the composition is specific for gp120. If a polyclonal antibody composition does not provide the desired specificity, the antibodies can be fractionated by ion exchange chromatography and immunoaffinity methods using intact gp120 or various fragments of gp120 to enhance specificity by a variety of conventional methods. For example, the composition can be fractionated to reduce binding to other substances by contacting the composition with gp120 affixed to a solid substrate. Those antibodies which bind to the substrate are retained. Fractionation techniques using antigens affixed to a variety of solid substrates such as affinity

chromatography materials including Sephadex, Sepharose and the like are well known.

Monoclonal anti-gp120 antibodies can be produced by a number of conventional methods. A mouse can be injected with an immunogenic composition containing gp120 and spleen cells obtained. Those spleen cells can be fused with a fusion partner to prepare hybridomas. Antibodies secreted by the hybridomas can be screened to select a hybridoma wherein the antibodies neutralize HIV infectivity, as described hereinafter. Hybridomas that produce antibodies of the desired specificity are cultured by standard techniques.

Infected human lymphocytes can be used to prepare human hybridomas by a number of techniques such as fusion with a murine fusion partner or transformation with EBV. In addition, combinatorial libraries of human or mouse spleen can be expressed in *E. coli* to produce the antibodies. Kits for preparing combinatorial libraries are commercially available. Hybridoma preparation techniques and culture methods are well known and constitute no part of the present invention. Exemplary preparations of monoclonal antibodies are described in the Examples.

Following preparation of anti-gp120 monoclonal antibodies, the antibodies are screened to determine those antibodies which are neutralizing antibodies. Assays to determine whether a monoclonal antibody neutralizes HIV infectivity are well known and are described in the literature. Briefly, dilutions of antibody and HIV stock are combined and incubated for a time sufficient for antibody binding to the virus. Thereafter, cells that are susceptible to HIV infection are combined with the virus/antibody mixture and cultured. MT-2 cells or H9 cells are susceptible to infection by most HIV strains that are adapted for growth in the laboratory. Activated peripheral blood mononuclear cells (PBMCs) or macrophages can be infected with primary isolates (isolates from a patient specimens which have not been cultured in T-cell lines or transformed cell lines). Daar et al, *Proc. Natl. Acad. Sci. USA* 87:6574-6578 (1990) describe methods for infecting cells with primary isolates.

After culturing the cells for about five days, the number of viable cells is determined, as by measuring metabolic conversion of the formazan MTT dye. The percentage of inhibition of infectivity is calculated to determine those antibodies that neutralize HIV. An exemplary preferred procedure for determining HIV neutralization is described in the Examples.

Those monoclonal antibodies which neutralize HIV are used to map the epitopes to which the antibodies bind. To determine the location of a gp120 neutralizing epitope, neutralizing antibodies are combined with fragments of gp120 to determine the fragments to which the antibodies bind. The gp120 fragments used to localize the neutralizing epitopes are preferably made by recombinant DNA methods as described hereinafter and exemplified in the Examples. By using a plurality of fragments, each encompassing different, overlapping portions of gp120, an amino acid sequence encompassing a neutralizing epitope to which a neutralizing antibody binds can be determined. A preferred exemplary determination of the neutralizing epitopes to which a series of neutralizing antibodies binds is described in detail in the Examples.

This use of overlapping fragments can narrow the location of the epitope to a region of about 20 to 40 residues. To confirm the location of the epitope and narrow the location to a region of about 5 to 10 residues, site-directed mutagenicity studies are preferably performed. Such studies can also determine the critical residues for binding of neutral-

izing antibodies. A preferred exemplary site-directed mutagenicity procedure is described in the Examples.

To perform site-directed mutagenicity studies, recombinant PCR techniques can be utilized to introduce single amino acid substitutions at selected sites into gp120 fragments containing the neutralizing epitope. Briefly, overlapping portions of the region containing the epitope are amplified using primers that incorporate the desired nucleotide changes. The resultant PCR products are annealed and amplified to generate the final product. The final product is then expressed to produce a mutagenized gp120 fragment. Expression of DNA encoding gp120 or a portion thereof is described hereinafter and exemplified in the Examples.

In a preferred embodiment described in Example 1, the gp120 fragments are expressed in mammalian cells that are capable of expression of gp120 fragments having the same glycosylation and disulfide bonds as native gp120. The presence of proper glycosylation and disulfide bonds provides fragments that are more likely to preserve the neutralizing epitopes than fragments that are expressed in *E. coli*, for example, which lack disulfide bonds and glycosylation or are chemically synthesized which lack glycosylation and may lack disulfide bonds.

Those mutagenized gp120 fragments are then used in an immunoassay using gp120 as a control to determine the mutations that impair or eliminate binding of the neutralizing antibodies. Those critical amino acid residues form part of the neutralizing epitope that can only be altered in limited ways without eliminating the epitope. Each alteration that preserves the epitope can be determined. Such mutagenicity studies demonstrate the variations in the amino acid sequence of the neutralizing epitope that provide equivalent or diminished binding by neutralizing antibodies or eliminate antibody binding. Although the amino acid sequence of gp120 used in the vaccine preferably is identical to that of a selected HIV isolate for the given geographic region, alterations in the amino acid sequence of neutralizing epitope that are suitable for use in a vaccine can be determined by such studies.

Once a neutralizing epitope is localized to a region of ten to twenty amino acids of gp120, the amino acid sequence of corresponding neutralizing epitopes of other HIV isolates can be determined by identifying the corresponding portion of the gp120 amino acid sequence of the isolate.

Once the neutralizing epitopes for a given region of gp120 are determined, the amino acid sequence of HIV isolates for the geographic region are determined. The complete amino acid sequence for numerous isolates has been determined and is available from numerous journal articles and in databases. In such cases, determination of the amino acid sequence of HIV isolates for the geographic region involves looking up the sequence in an appropriate database or journal article. However, for some isolates, the amino acid sequence information does not include the sequence of the V2 or C4 domains.

When the amino acid sequence of a region of interest for a given isolate is not known, the amino acid sequence can be determined by well known methods. Methods for determining the amino acid sequence of a protein or peptide of interest are well known and are described in numerous references including Maniatis et al., *Molecular Cloning—A Laboratory Manual*, Cold Spring Harbor Laboratory (1984). In addition, automated instruments which sequence proteins are commercially available.

Alternatively, the nucleotide sequence of DNA encoding gp120 or a relevant portion of gp120 can be determined and the amino acid sequence of gp120 can be deduced. Methods

for amplifying gp120-encoding DNA from HIV isolates to provide sufficient DNA for sequencing are well known. In particular, Ou et al, *Science* 256:1165–1171 (1992); Zhang et al. *AIDS* 5:675–681 (1991); and Wolinsky *Science* 255:1134–1137 (1992) describe methods for amplifying gp120 DNA. Sequencing of the amplified DNA is well known and is described in Maniatis et al., *Molecular Cloning—A Laboratory Manual*, Cold Spring Harbor Laboratory (1984), and Horvath et al., *An Automated DNA Synthesizer Employing Deoxynucleoside 3'-Phosphoramidites*, *Methods in Enzymology* 154: 313–326, (1987), for example. In addition, automated instruments that sequence DNA are commercially available.

In a preferred embodiment, the isolate is a patient isolate which has not been passaged in culture. It is known that following passage in T-cells, HIV isolates mutate and isolates best suited for growth under cell culture conditions are selected. For example, cell culture strains of HIV develop the ability to form syncytia. Therefore, preferably the amino acid sequence of gp120 is determined from a patient isolate prior to growth in culture. Generally, DNA from the isolate is amplified to provide sufficient DNA for sequencing. The deduced amino acid sequence is used as the amino acid sequence of the isolate, as described hereinbefore.

To determine the percentage each isolate constitutes of total HIV that infects individuals in the geographic region, standard epidemiological methods are used. In particular, sufficient isolates are sequenced to ensure confidence that the percentage of each isolate in the geographic region has been determined. For example, Ichimura et al, *AIDS Res. Hum. Retroviruses* 10:263–269 (1994) describe an epidemiological study in Thailand that determined that there are two strains of HIV present in the region. HIV strains have only recently been present in Thailand and Thailand, therefore has the most homogenous population of HIV isolates known to date. The study sequenced 23 isolates from various parts of the country and determined that only two different amino acid sequences were present in the isolates.

In contrast, HIV has been infecting individuals in Africa for the longest period of any geographic region. In Africa, each of the most common isolates probably constitutes about 5% of the population. In such cases, more isolates would need to be sequenced to determine the percentage each isolate constitutes of the population. Population studies for determining the percentage of various strains of HIV, or other viruses, present in a geographic region are well known and are described in, for example, Ou et al, *Lancet* 341:1171–1174 (1993); Ou et al, *AIDS Res. Hum. Retroviruses* 8:1471–1472 (1992); and McCutchan et al., *AIDS Res. Hum. Retroviruses* 8:1887–1895 (1992).

In the United States and western Europe, probably about two to four different neutralizing epitopes in each of the V2, V3, and C4 domains constitute 50 to 70% of the neutralizing epitopes for each domain in the geographic region, as described more fully hereinafter.

Selection Method

Once the amino acid sequence of neutralizing epitopes for strains in a region are determined, gp120 from an HIV strain having gp120 that has an amino acid sequence for a neutralizing epitope in the V2 or C4 domain which sequence is one of the most common in the geographic region is selected. One of the most common neutralizing epitope amino acid sequences means that the strain has an amino acid sequence for at least one neutralizing epitope that is occurs among the most frequently for HIV isolates in the geographic region and thus is present as a significant percentage of the population. For example, if there are three

sequences for a neutralizing epitope that constitute 20, 30, and 40 percent of the sequences for that epitope in the region and the remainder of the population is comprised by 2 to 4 other sequences, the three sequences are the most common. Therefore, in African countries, if each of several amino acid sequences constitute about 5% of the sequences for a neutralizing epitope and the remainder of the sequences each constitute less than 1% of the population, the isolates that constitute 5% of the population are the most common.

Preferably, isolates having the most common amino acid sequences for a neutralizing epitope are chosen. By the most common is meant that the sequences occur most frequently in the geographic region. For example, in the United States, the MN isolate has a C4 neutralizing epitope that comprises at least about 45% of the population. The GNE₈ isolate has a C4 neutralizing epitope that comprises at least about 45% of the population. Thus either isolate has the most common C4 neutralizing epitope in the region. When gp120 from each isolate is combined in a vaccine, greater than about 90% of the C4 neutralizing epitope sequences are present in the vaccine. In addition, the amino acid sequences for the V3 neutralizing epitope in the MN and GNE₈ isolates are substantially similar and comprise about 60% of the population. Therefore, those strains have the two most common neutralizing epitopes for the V3 domain. In the V2 region, the MN isolate amino acid sequences comprises about 10% of the population, and the GNE₈ isolate amino acid sequences comprises about 60% of the population. Therefore, the GNE₈ strain has the most common neutralizing epitope for the region and the two strains together comprise the two most common neutralizing epitopes for the region. A multivalent gp120 subunit vaccine containing the two isolates contains amino acid sequences for epitopes that constitute about 70% of the V2 domain, about 60% of the V3 domain, and about 90% of the C4 domain for the United States.

In a preferred embodiment of the method, one or more HIV isolates having an amino acid sequence for a neutralizing epitope in the V2 and/or C4 domains that constitute at least about 50% of the population for a selected geographic region are selected. In a more preferred embodiment, isolates having the most common neutralizing epitopes in the V3 domain are also included in the vaccine.

As is clear, once the most common amino acid sequences for the neutralizing epitopes in the V2, V3, and C4 domains are known, an isolate having a common epitope for each region is preferably selected. That is, when only two or three isolates are used for the vaccine, it is preferable to select the isolate for common epitopes in each region, rather than selecting an isolate by analysis of a single region.

In a more preferred embodiment, gp120 from isolates having epitopes that constitute at least 50% of the population for the geographic region for V2, V3, and C4 domains are present in the vaccine. More preferably, the isolates have epitopes that constitute at least 60% of the population for the geographic region for the three domains. Most preferably, 70% or more are included.

In another preferred embodiment, the entire amino acid sequence of the V2 and C4 domains is determined in the selection process. In addition to selecting common sequences for the neutralizing epitopes, isolates having unusual polymorphisms elsewhere in the region are preferably not used for the vaccine isolates.

Vaccine Preparation

gp120 from the selected HIV isolate(s) is used to make a subunit vaccine, preferably a multivalent subunit vaccine. Preparation of gp120 for use in a vaccine is well known and

is described hereinafter. With the exception of the use of the selected HIV isolate, the gp120 subunit vaccine prepared in the method does not differ from gp120 subunit vaccines of the prior art.

As with prior art gp120 subunit vaccines, gp120 at the desired degree of purity and at a sufficient concentration to induce antibody formation is mixed with a physiologically acceptable carrier. A physiologically acceptable carrier is nontoxic to a recipient at the dosage and concentration employed in the vaccine. Generally, the vaccine is formulated for injection, usually intramuscular or subcutaneous injection. Suitable carriers for injection include sterile water, but preferably are physiologic salt solutions, such as normal saline or buffered salt solutions such as phosphate buffered saline or ringer's lactate. The vaccine generally contains an adjuvant. Useful adjuvants include QS21 which stimulates cytotoxic T-cells and alum (aluminum hydroxide adjuvant). Formulations with different adjuvants which enhance cellular or local immunity can also be used.

Addition excipients that can be present in the vaccine include low molecular weight polypeptides (less than about 10 residues), proteins, amino acids, carbohydrates including glucose or dextrans, chelating agents such as EDTA, and other excipients.

The vaccine can also contain other HIV proteins. In particular, gp41 or the extracellular portion of gp41 can be present in the vaccine. Since gp41 has a conserved amino acid sequence, the gp41 present in the vaccine can be from any HIV isolate. gp160 from an isolate used in the vaccine can replace gp120 in the vaccine or be used together with gp120 from the isolate. Alternatively, gp160 from an isolate having a different neutralizing epitope than those in the vaccine isolates can additionally be present in the vaccine.

Vaccine formulations generally include a total of about 300 to 600 μ g of gp120, conveniently in about 1.0 ml of carrier. The amount of gp120 for any isolate present in the vaccine will vary depending on the immunogenicity of the gp120. For example, gp120 from the Thai strains of HIV are much less immunogenic than gp120 from the MN strain. If the two strains were to be used in combination, empirical titration of the amount of each virus would be performed to determine the percent of the gp120 of each strain in the vaccine. For isolates having similar immunogenicity, approximately equal amounts of each isolate's gp120 would be present in the vaccine. For example, in a preferred embodiment, the vaccine includes gp120 from the MN, GNE₈, and GNE₁₆ strains at concentrations of about 300 μ g per strain in about 1.0 ml of carrier. Methods of determining the relative amount of an immunogenic protein in multivalent vaccines are well known and have been used, for example, to determine relative proportions of various isolates in multivalent polio vaccines.

The vaccines of this invention are administered in the same manner as prior art HIV gp120 subunit vaccines. In particular, the vaccines are generally administered at 0, 1, and at 6, 8 or 12 months, depending on the protocol. Following the immunization procedure, annual or bi-annual boosts can be administered. However, during the immunization process and thereafter, neutralizing antibody levels can be assayed and the protocol adjusted accordingly.

The vaccine is administered to uninfected individuals. In addition, the vaccine can be administered to seropositive individuals to augment immune response to the virus, as with prior art HIV vaccines. It is also contemplated that DNA encoding the strains of gp120 for the vaccine can be administered in a suitable vehicle for expression in the host. In this way, gp120 can be produced in the infected host,

eliminating the need for repeated immunizations. Preparation of gp120 expression vehicles is described hereinafter.
Production of gp120

gp120 in the vaccine can be produced by any suitable means, as with prior art HIV gp120 subunit vaccines. Recombinantly-produced or chemically synthesized gp120 is preferable to gp120 isolated directly from HIV for safety reasons. Methods for recombinant production of gp120 are described below.

DNA Encoding GNE₈ and GNE₁₆ gp120 and the Resultant Proteins

The present invention also provides novel DNA sequences encoding gp120 from the GNE₈ and GNE₁₆

isolates which can be used to express gp120 and the resultant gp120 proteins. A nucleotide sequence of less than about 5 kilobases (Kb), preferably less than about 3 Kb having the nucleotide sequence illustrated in Tables 1 and 2, respectively, encodes gp120 from the GNE₈ and GNE₁₆ isolates. The sequences of the genes and the encoded proteins are shown below in Tables 1–3. In particular, Table 1 illustrates the nucleotide sequence (SEQ. ID. NO. 27) and the predicted amino acid sequence (SEQ. ID. NO. 28) of the GNE₈ isolate of HIV. The upper sequence is the coding strand. The table also illustrates the location of each of the restriction sites.

TABLE 1

1	ATGATAGTGA AGGGGATCAG GAAGAATTGT CAGCACTTGT GGAGATGGG CACCATGCTC CTGGGATGT TGATGATCTG TAGTGTCTGCA GAAAAATTGT TACTATCACT TCCCCTAGTC CTTCTTAACA GTCGTGAACA CCTCTACCCG GTGGTACGAG GAACCCCTACA ACTACTAGAC ATCACGACGT CTTTTTAACA 1 M I V K G I R K N C Q H L W R W G T M L L G M L M I C S A A E K L W	hgici bani bsp1286 bmyI styI scfI bsgI
	kpnI hgici bani asp718 acc65I	
101	GGGTACAGT CTATTATGG GTACCTGTGT GGAAGAAGC AACCCACT CTATTTTGTG CATCAGATGC TAAAGCATAT GATACAGAGG TACATAATGT CCCAGTCA GATAATACCC CATGGACACA CCTTCTTCG TTGGTGGTGA GATAAAACAC GTAGTCTACG ATTTCCGTATA CTATGTCTCC ATGTAATTACA 35 V T V Y Y G V P V W K E A T T T L F C A S D A K A Y D T E V H N V	ndeI
	nspI nspHI nspHI	
201	TTGGGCCACA CATGCCCTGT TACCCACAGA CCCCACCCCA CAAGAATAG GATTGAAAA TGTAAACAGAA AATTTTAAACA TGTGGAAAA TAACATGGTA AACCCGTGT GTACGGACAC ATGGGTGTCT GGGGTGGGT GTTCTTTATC CTAACTTTT ACATTTCTT TTAATAATTGT ACACCTTTT ATTTGACCAT 68 W A T H A C V P T D P N P Q E I G L E N V T E N F N M W K N N M V	apoi nspI nspHI afIII
	ppu10I nsii/avaIII hindIII	
301	GACAGATGC ATGAGGATAT AATCAGTTTA TGGGATCAAA GCTTAAAGCC ATGTGTAATA TTAACCCAC TATGTGTAC TTTAAATTGC ACTGATTTGA CTTGTACAG TACTCCATA TTAGTCAAT ACCCTAGTT CGAATTTCCG TACACATTT AATTTGGGTG ATACACATG AATTTAACG TGACTAACT 101 E Q M H E D I I S L W D Q S L K P C V K L T P L C V T L N C T D L K	draIII ahaIII/draI
	pvuII speI nspBII	
401	AAAATGCTAC TAATACCACT AGTAGCAGT GGGGAAAGAT GGAGAGAGG AAAAAAATA ACTGCTCTT CAATGTCAC ACAAGTATAA GAGATAAGAT TTTTACGATG ATTATGGTGA TCATCGTGA CCCCTTTCTA CCTCTCTCT CTTTATTTT TGACGAGAAA GTTACAGTGG TGTTCATATT CTCTATTCTA 135 N A T N T T S S S W G K M E R G E I K N C S F N V T T S I R D K M	
	scfI	
501	GAGAATGAA TATGCACTTT TTTATAAACT TGATGTAGTA CCAATAGATA ATGATAATAC TAGTATAGG TTGATAAGTT GTAACACCTC AGTCAATTACA CTTCTTACTT ATACGTGAAA AATAATTTGA ACTACATCAT GGTATATAT TACTATATAT ATCGATATCC AACTATTCAA CATTTGGAG TCAGTAAATG 168 K N E Y A L F Y K L D V V P I D N D N T S Y R L I S C N T S V I T	
	stuI haeI	
601	CAGGCTGTC CAAAGGTGTC CTTTGAGCCA ATTCCCATAC ATTATTTGTC CCCGGTGGT TTTGGATTG TAAAGTGTAG AGATAAAAAG TTCAACCGGAA GTCCGGACAG GTTCCACAG GAAACTCGGT TAAAGGTATG TAATAACAG TAATACAGCA AACCGTAAAG ATTTTCAATC TCTATTTTC AAGTTGCCTT 201 Q A C P K V S F E P I P I H Y C A P A G F A I L K C R D K K F N G T	bsp1286 bmyI
	bsp1407I haeI	
701	CAGGACCATG TACAAATGTC AGCAGATAC AATGTACACA TGGAAATAGG CAGTAGTAT CAACTCAACT GCTGTTAAT GGCAGTTTAG CAGAAGAAGA GTCCGTGATC ATGTTTACAG TCGTGTCTAG TTACATGTT ACCTTAATCC GGTCAATCA GGTGATGTA GTTGAATTA CCGTCAAAATC GTCTTCTTCT 235 G P C T N V S T V Q C T H G I R P V V S T Q L L N G S L A E E	

TABLE 1-continued

bstYI/xhoII pvuII bsp1407I
 bg111 nspBII aseI/asnI/vspI
 801 AGTAGTAATT AGATCTGCCA ATTTCTCGGA CAATGCTAAA ACCATAATAG TACAGCTGAA CGAATCTGTA GAAATTAATT GTACAAGACC CAACAACAAT
 TCATCAATTA TCTAGACGGT TAAAGAGCCT GTTACGATTT TGGTATTATC ATGTCGACTT GCTTAGACAT CTTTAAITTA CATGTTCTGG GTTGTGTTA
 268 V V I R S A N F S D N A K T I I V Q L N E S V E I N C T R P N N N

 bst1107I accI
 901 ACAAGAAGAA GTATACATAT AGGACCAGG AGAGCATTTT ATGCAACAGG AGAATAATA GGAGACATA GACAAGCACA TTGTAACCTT AGTAGCACA
 TGTTCCTCTT CATATGTATA TCCCTGGTCCC TCTCGTAAAA TACGTTGTCC TCTTTATAT TCTCTGTATT CTGTTCTGT AACTTGGAA TCATCGTGT
 301 T R R S I H I G P G R A F Y A T G E I I G D I R Q A H C N L S S T K

 ahaIII/draI ppuMI
 1001 AATGGAATA TACTTTAAA CAGATAGTTA CAAAATTAAG AGAACATTTT AATAAACA TAGTCTTTAA TCACTCTCA GGAGGGACC CAGAAATTTGT
 TTACCCTATT ATGAAATTTT GTCTATCAAT GTTTTAAATC TCTTGTAATA TTAATTTGTT ATCAGAAAT AGTGAGGAGT CCTCCCTGG GTCTTTAACA
 335 W N N T L K Q I V T K L R E H F N K T I V F N H S S G G D P E I V

 apoI scaI
 1101 AATGACAGT TTTAATTGT GAGGGAAAT TTTCTACTGT AATACAAC CACTGTTTAA TAGTACTGG AATTATACTT ATACTGGAA TAATACTGAA
 TTACGTGTCA AAATTAACAC CTCCCCTTAA AAAGATGACA TTAATGTTGT GTGACAAAT ATCATGAACC TTAATATGAA TATGAACCTT ATTATGACTT
 368 M H S F N C G G E F F Y C N T T P L F N S T W N Y T Y T W N N T E

 nspI nspHI
 1201 GGTCAAATG AACTTGAAG AAATATACA CTCCAATGCA GAATAAACA AATATAAAC ATGTGGCAGG AAGTAGGAAA AGCAATGTAT GCCCTCCCA
 CCCAGTTAC TGTGACCTTC TTTATAGTGT GAGGTTACGT CTTATTTTGT TTAATATTG TACACCGTCC TTCATCCTTT TCGTTACATA CGGGGAGGGT
 401 G S N D T G R N I T L Q C R I K Q I I N M W Q E V G K A M Y A P P I

 mami eeo57I
 bsaBI sspI bstYI/xhoII gsuI/bpmI
 1301 TAAGAGACA AATTAGATGC TCATCAATA TACAGGGCT GCTATTAACA AGAGATGGT GTAATAACAG CGAAACCAG ATCTTCAGAC CTGGAGGAGG
 AFTCTCCTGT TTAATCTACG AGTAGTTTAT AATGTCCCGA CGATAAATGT TCTCTACCAC CATTATTGTC GCTTTGGTC TAGAAGTCTG GACCTCCTCC
 435 R G Q I R C S S N I T G L L L T R D G G N N S E T E I F R P G G G

 munI styI earI/ksp632I
 1401 AGATATGAG GACAATGGA GAAGTGAAT ATATAAATAT AAAGTAGTAA AATTTGAACC ATTAGGAGTA GCACCCACCA AGGCAAAGAG AAGAGTGATG
 TCTATACTCC CTGTTAACCT CTTCACITTA TATATTATA TTTTCACTAT TTTTAACTGG TAATCCTCAT CGTGGTGGT TCCGTTTCTC TTCTCACATC
 468 D M R D N W R S E L Y K Y K V V K I E P L G V A P T K A K R R V M

 styI
 1501 CAGAGAGAA AAAGAGCAGT GGAATAGGA GCTGTGTTCC TTGGTTCCTT GAGCAGCA GGAAGCACTA TGGCGGAGC GTCAGTGACG CTGACGGTAC
 GTCTCTCTT TTTCTCGTCA CCTTTATCCT CGACACAAGG AACCCAAGAA CCTTCGTCGT CCTTCGTGAT ACCCGCGTGC CAGTCACTGC GACTGCCATG
 501 Q R E K R A V G I G A V F L G F L G A A G S T M G A A S V T L T V Q

 haeI alwNI
 1601 AGGCCAGACT ATTATTGCT GGTATAGTC AACAGCAGAA CAATTTGCTG AGGGTATTG AGCCGAACA GCATCTGTTG CAACTCACAG TCTGGGGCAT
 TCCGGTCTGA TAATAACAGA CCATATCAG TTGTCGTCTT GTTAAACGAC TCCCGATAAC TCCGGCTTGT CGTAGACAAC GTTGAGTGTG AGACCCCGTA

TABLE 1-continued

535	A R L L L S G I V Q Q Q N N L L R A I E A E Q H L L Q L T V W G I
1701	gsuI/bpmI CAAGCAGCTC CAGGCAAGAG TCCTGGCTGT GGAGAGATAC CTAAGAGATC GGGGATTTGG GGTTCCTCTG GAAAACTCAT CTGCACCACCT GTTCCGTCGAG GTCCGTTCTC AGGACCGACA CCTCTCTATG GATTTCCTAG TTGTCGAGGA CCCCTAAACC CCAACGAGAC CTTTGTGAGTA GACGTGGTGA
568	K Q L Q A R V L A V E R Y L K D Q Q L L G I W G C S G K L I C T T
1801	styI bsmI GCTGTGCCCTT GGAATGCTAG TTGGAGTAAAT AAATCTCTGG ATAAGATTTG GGAATAACATG ACCTGGATGG AGTGGGAAAG AGAAATTTGAC AATTACACAA CGACACGGAA CCTTACGATC AACCTCAITTA TTAGAGACC TATTCTAAAC CCTATTGTAC TGGACCTACC TCACCCCTTTC TCTTTAACTG TTAATGTGTT
601	A V P W N A S W S N K S L D K I W D N M T W M E W E R E I D N Y T S
1901	GCTTAAATATA CAGCTTAAT GAAGAATCGC AGAACCAACA AGAAAAAAT GAACAAGAAT TATTGGAAT AGATAAATGG GCAAGTTTGT GGAATTTGTT CGAATTATAT GTCGAATTAA CTTCTTAGCG TCTTGGTTGT TCTTTTTTTA CTTGTTCTTA ATAACCTTAA TCTATTTACC CGTTCAAAACA CCTTAAACCAA
635	L I Y S L I E E S Q N Q Q E K N E Q E L L E L D K W A S L W N W F
2001	scfI TGACATAACA AAATGGCTGT GGTATATAAA AATATTGATA ATGATAGTAG GAGGCTTGGT AGTTTAAAGA ATAGTTTTTA CTGTACTTTC TATAGTGAAT ACTGTATTGT TTTACCGACA CCATATATTT TTATAAGTAT TACTATCATC CTCGGAACCA TCCAAATICT TATCAAAAAT GACATGAAAG ATATCACITTA
668	D I T K W L W Y I K I F I M I V G G L V G L R I V F T V L S I V N
2101	avaI AGAGTTAGGA AGGATACCTC ACCATTATCG TTCCAGACCC ACCTCCCAGC CTCGACAGGC CCGAAGGAA CCGAAGAAGAA GGTGGAGAGC TCTCAATCCT TCCCTATGAG TGGTAAATAGC AAGGTCTGGG TGGAGGCTCG GGGTCCCTT GAGCTGTCCG GGTTCCTCTG GCTTCTTCTT CCACCTCTCG
701	R V R K G Y S P L S F Q T H L P A P R G L D R P E G T E E E G E R
735	D R D R S S R L V D G F L A I V W V D L R S L C L F S Y H R L R D
2201	bspMI GAGACAGAGA CAGATCCAGT CGATTAGTG AGGATTTCTT AGCAATGTC TGGTTCGACC TGCAGGACCT TGCAGGACCT GTGCCCTTTC AGCTACCACC GCTTGAGAGA CTCTGTCTCT GTCTAGGTCA GCTAATCAC TACCTAAGAA TCGTTAACAG ACCCAGCTGG ACGCTTCGGA CACGGAGAA TCGATGGTGG CGAACTCTCT
2301	scfI CTTACTCTTG ATTGCAGCGA GGATTTGGA ACTTCTGGGA CGCAGGGGGT GGGAAAGCCCT CAAATATTGG TGGAAATCTCC TACAGTATTG GATTCAGGAA GAATGAGAAC TAACTGCTGCT CCTAACACCT TGAAGACCCCT GCGTCCCCCA CCTTTCGGGA GTTTATAACC ACCTTAGAGG ATGTCATAAC CTAAGTCTT
768	L L L I A A R I V E L L G R R G W E A L K Y W W N L L Q Y W I Q E
2401	alwNI CTAAGAATA GTGCTGTTAG CTTGCTCAAT GCCACAGCCA TAGCAGTAGC TGAGGGAACA GATAGGGTTA TAGAAATAGT ACAAGAGCT TATAGAGCTA GATTTCTTAT CACGACAATC GAACGAGTTA CCGTGTGGT ATCGTCATCG ACTCCCTGT CTATCCCAAT ATCTTTATCA TGTTCCTCGA ATATCTCGAT
801	L K N S A V S L L N A T A I A V A E G T D R V I E I V Q R A Y R A I
2501	TTCTCCACAT ACCCACAGA ATAAGACAGG GCTTGGAAAG GGCTTTGCTA TAA AAGAGGTGTA TGGGTGCTT TATTCTGTCC CGAACCTTTC CCGAAACGAT ATT
835	L H I P T R I R Q G L E R A L L O

Table 2 illustrates the nucleotide sequence and the predicted amino acid sequence of the GNE₁₆ isolate of HIV. The upper sequence is the coding strand. The table also illustrates the location of each of the restriction sites. The first four pages of the table are from one clone of the gene and the second three pages of the table are from another

clone of the gene. The sequences of the clones differ by about 2%. (The nucleotide sequences are SEQ. ID. NOS. 29 and 31, respectively. The amino acid sequences are SEQ. ID. NOS. 30, 32 and 33.) It is noted that each of the sequences includes a stop codon. A gene sequence that encodes full length gp120 can be made by repairing one of the sequences.

TABLE 2

	hgici	scfi
	banI	pstI
	bsp1286	bsgI
	bmyI	scfi
	styI	
1	ATGAGACTGA AGGGATCAG GAGGAATTAT CAGCACTTGT GGAGATGGG CACCATGCTC CTTGGGATAT TGATGATCTG TAGTGTCTGA GGGAAATTGT	
	TACTTCACT TCCCTTAGTC CTCCTTAATA GTCGTGAACA CCTCTACCC GTGGTACGAG GAACCCATA ACTACTAGAC ATCAGGACGT CCCTTTAACA	
1	M R V K G I R R N Y Q H L W R W G T M L L G I L M I C S A A G K L W	
	kpnI	
	hgici	
	banI	
	asp718	
	acc65I	
101	GGGTACAGT CTATTATGG GTACCTGTGT GGAAGAAGAAC AACACCACCT CTATTTTGTG CATCAGATGC TAAAGCATAT GATACAGAGA TACATAATGT	
	CCCAGTCTCA GATAATACCC CATGGACACA CCTTCTTTTG TTGGTGGTGA GATAAAACAC GTAGTCTACG ATTTCCGTATA CTATGTCTCT ATGTAATTACA	
35	V T V Y Y G V P V W K E T T T T L F C A S D A K A Y D T E I H N V	
	ndeI	
	nspI	
	nspHI	
	afIII	
	apoI	
201	TTGGGCCACA CATGCCCTGT TACCCACAGA CCCCACCCCA CAAGAAGTAG TATTGAAAAA TGTGACAGAA AATTTTAAACA TGTGGAAAAA TAACATGGTG	
	AACCCGGTGT GTACGGACAC ATGGGTGTCT GGGGTGGGT GTTCTTCACT ATAACCTTTT ACACGTCTT TTAATAATTGT ACACCTTTT ATTTGACCAC	
68	W A T H A C V P T D P N P Q E V V L E N V T E N F N M W K N N M V	
	ppu10I	
	nsII/avaIII	
	ahaIII/draI	
	ahaIII/draI	
301	GACACAGTGC ATGAGGATAT AATCAGTTTA TGGGATCAAA GTTTAAAGCC ATGTGTAAA TTAACCCAC TCTGTGTAC TTTAAATTGC ACTGATGCCG	
	CTTGTCTACG TACTCCTATA TTAGTCAAT ACCCTAGTTT CAAATTTCCG TACACATTTT AATTTGGGTG AGACACATG AATTTAACC TGACTACGCC	
101	E Q M H E D I I S L L W D Q S L K P C V K L T P L C V T L N C T D A G	
	gsuI/bpmI	
401	GGAACTACTAC TAATACCAAT AGTAGTAGCA GGGAAAAGCT GGAGAAAAGG GAAATAAAAA ACTGCTCTT CAATATCACC ACAAGCGTGA GAGATAAGAT	
	CCTTATGATG ATTATGGTTA TCATCATCGT CCCTTTTCGA CCTCTTTCCT CTTTATTTT TGACGAGAAA GTTATAGTGG TGTTCGCACT CTCTATTCTA	
135	N T T N T N S S S R E K L E K G E I K N C S F N I T T S V R D K M	
	421,reverse	
501	GCAGAAAAGAA ACTGCACCTT TTAATAAACT TGATATAGTA CCAATAGATG ATGATGATAG GAATAGTACT AGGAATAGTA CTAACATATAG GTTGATAAGT	
	CGTCTTCTT TGACGTGAAA AATTAATTGA ACTATATCAT GGTATCTAC TACTACTATC CTATCATGA TCCTTATCAT GATGATATC CAACTATTCA	
168	Q K E T A L F N K L D I V P I D D D R N S T R N S T N Y R L I S	
	43r2,reverse	
601	TGTAACACCT CAGTCATTAC ACAGGCCCTGT CCAAAGGTAT CATTGAGCC AATTCACATA CATTCTGTA CCCCAGCTGG TTTTGGCTT CTAAAAGTGA	
	ACATTTGGGA GTCAGTAATG TGTCCGGACA GGTTCACATA GTAAACTCG TTAAGGTAT GTAAAGACAT GGGCCGACC AAAACGCGAA GATTTTCACAT	
201	C N T S V I T Q A C P K V S F E P I P I H F C T P A G F A L L K C N	
	stuI	
	haeI	
701	ATAATAAGAC GTTCAATGGA TCAGGACCAT GCAAAAATGT CAGCACAGTA CAAATGACAC ATGGAATTAG GCCAGTAGTA TCAACTCAAC TGCTGTTAAA	
	TATTTATCTG CAAGTTACCT AGTCCCTGGTA CGTTTTTACA GTCGTGTCAT GTTACATGTG TACCTTAAIC CCGTCAATCAT AGTTGAGTTG ACGACAAATTT	

TABLE 2-continued

235	N K T F N G S G P C K N V S T V Q C T H G I R P V V S T Q L L L N		
		bstYI/xhoII bglIII apoI	pvuII nspBII aseI/asnI/vspI
801	TGGCAGTCTA GCAGAAGGAG AGGTAGTAAAT TAGACTGAA AATTTCACGA ACATGCTAA AACATAATA GTACAGCTGA CAGAACCAGT AAAAAATTAAT ACCGTCAGAT CGTCTTCCCTC TCCATCAITTA ATCTAGACTT TTAAGTGTCT TTTACGATTT TGGTATAT CATGTCGACT GCTTGGTCA TTTTAAATTA		
268	G S L A E G E V I R S E N F T N A K T I I V Q L T E P V K I N		
			^fl,forward
		bst1107I accI scfI	
901	TGTACAAGAC CCAACAACA TACAAGAAA AGTATACCTA TAGGACCAGG GAGAGCATTT TATGCAACAG GAGACATAAT AGGAAATATA AGACAAGCAC ACATGTTCTG GGTGTGTGTT ATGTTCTTTT TCATATGGAT ATCCTGGTCC CTCCTGTAATA ATACGTTGTC CTCCTGTAATA TCCTTTATAT TCTGTTCGTG		
301	C T R P N N T R K S I P I G P G R A F Y A T G D I I G N I R Q A H		
		875,reverse	
		ppuMI eco0109I/draII	eco81I bsu36I/mstII/sauI
1001	ATTTGTAACCT TAGTAGAACA GACTGGAATA ACACTTTAGG ACAGATAGTT GAAAAATTA GAGAACAATT TGGGAATAAA ACAATAATCT TTAATCACTC TAACATTTGA ATCATCTTGT CTGACCTTAT TGTGAAATCC TGTCTATCAA CTTTTTAATTT CTCTTGTAA ACCCTTATTT TGTATATAGA AATTAGTGAG		
335	C N L S R T D W N N T L G Q I V E K L R E Q F G N K T I I F N H S		
		munI apoI scaI	
1101	CTCAGGAGG GACCCAGAAA TTGTAATGCA CAGTTTTAAT TGTAGAGGGG AATTTTTCTA CTGTAATACA ACACAATTTG TTGACAGTAC TTGGGATAAT GAGTCTCCC CTGGTCTTT AACATTTACG GTCAAAAATTA ACATCTCCCC TTAATAAAGAT GACATTTATG TGTGTTACA AACTGTCATG AACCCATATA		
368	S G G D P E I V M H S F N C R G E F F Y C N T T Q L F D S T W D N		
		earI/ksp632I eco57I	nspI nspHI afIII
1201	ACTAAAGTGT CAAATGGCAC TAGCCTGAA TAGAATAGCA CAATCACACT CCCATGCAGA ATAAAGCAA TTGTAACAAT GTGGCAGGAA GTAGGAAAAG TGATTTTACA GTTTACCGTG ATCGTGACTT CTCCTTATCGT GTTAGTGTGA GGGTACGCTT TATTTGTTT AACATTTGTA CACCGTCTTT CATCCITTTT		
401	T K V S N G T S T E E N S T I T L P C R I K Q I V N M W Q E V G K A		
		mamI bsaBI sspI	bsaI
1301	CAATGTATGC CCTCCCATC AGAGGACAAA TTAGATGTTT ATCAATATTT ACAGGTTGC TATTAACAAG AGATGGAGGT AGTAACAACA GCATGAATGA GTTACATACG GGGAGGGTAG TCTCCTGTTT AATCTACAAG TAGTTTATAA TGTCCCAACG ATAAATGTTT TCTACCTCCA TCATTTGTTG CGTACTTACT		
435	M Y A P P I R G Q I R C S S N I T G L L L T R D G G S N N S M N E		
		2,16.7f3,forward	
		gsuI/bpmI eco57I munI	styI
1401	GACCTTCAGA CCTGGAGGAG GAGATATGAG GGACAATTTG AGAAGTGAAT TATACAATA TAAAGTAGTA AAAATTGAAC CATTAGGAGT AGCACCACC CTGGAAGTCT GGACCTCCTC CTCATATAC CTCCTGTTAAC CCTGTTAAC ATATGTTTAT ATTTCAATCAT TTTTAACTTG GTAATCCTCA TCGTGGGTGG		
468	T F R P G G D M R D N W R S E L Y K Y K V V K I E P L G V A P T		
		c4rev4,reverse	
		earI/ksp632I	styI
1501	AAGGCAAGA GAAGAGTGT GCAGAGAGAA AAAAGAGCAG TGGGAATAGG AGCTGTGTTCT TGGGTTCT TAGGAGCAG AGGAAGCACT ATGGGCGCAG TTCCGTTTCT CTCTCACCA CGTCTCTCTT TTTTCTGTC ACCCTTATCC TCGACACAAG GAACCCAAG ATCCTCGTCG TCCCTCGTGA TACCCGCGTC		

TABLE 2-continued

501	K A K R R V V Q R E K R A V G I G A V F L G F L G A A G S T M G A A	
1601	CGTCAATAAC GCTGACGGTA TATTATTGTC TGGTATAGTG CAACAGCAGA ACAATTTGCT GAGGGCTATT GAGGGCGAAC AGCATCTGTT GCAGTTATTG CGACTGCCAT GTCCGGTCTG ATAATAACAG ACCATATCAC GTTTCGCTCT TGTAAACGA CTCCCGATAA CTCCGGCTTG TCGTAGACAA	haeI
535	S I T L T V Q A R L L L S G I V Q Q Q N N L L R A I E A Q Q H L L	alwNI
		^ 43f5, forward
		^ 43r3, reverse
1701	GCAACTCATA GTCTGGGCA TCAAGCAGCT CCAGGCAAGA GTCCTGGCTG TGGAAAGATA CCTAAGGGAT CAACAGCTCC TGGGGATTG GGGTTGCTCT CGTTGAGTAT CAGACCCCGT AGTTCGTCGA GGTCCGTTCT CAGGACCGAC ACCTTCTAT GGATTCCTA GTTGTGAGG ACCCCATAAC CCCAACGAGA	gsuI/bpmI
568	Q L I V W G I K Q L Q A R V L A V E R Y L R D Q Q L L G I W G C S	eco81I alwNI bsu36I/mstII/sauI
1801	GGAAACTCA TTTGCACCAC CTCAGTGCCT TGGAAATGCTA GTTGGAGTAA TAAATCTCTA GATAAGATTT GGGATAACAT GACCTGGATG GAGTGGGAAA CCTTTTCAGT AAACGTGGTG GAGTCACGGA ACCTTACGAT CAACCTCATT ATTTAGAGAT CTATTTCTAAA CCTATTGTA CTGGACCTAC CTCACCCCTTT	styI bsmI xbaI
601	G K L I C T T S V P W N A S W S N K S L D K I W D N M T W M E W E R	
1901	GAGAAATTGA GAATTACACA AGCTTAAATAT ACACCTTAAT TGAAGAATCG CAGAACCAAC AAGAAAAGAA TGAACAAGAC TTATTGGAAT TGGATCAATG CTCTTTAACT CTTAATGTGT TCGAATTATA TGTGGAATTA ACTTCITAGC GTCITGGTTG TTTCTTTCTT ACTTGTTCG AATAACCTTA ACCTAGTTAC	hindIII
635	E I E N Y T S L I Y T L I E E S Q N Q Q E K N E Q D L L E L D Q W	
2001	GGCAAGTCTG TGAATTTGGT TTAGCATAAC AAAATGGCTG TGGTATATAA AATATTTCAT AATGATAGTT GGAGGCTTGG TAGGTTAAG AATAGTTTTT CCGTTACAGAC ACCTTAACCA AATCGTATTG TTTTACCGAC ACCATATATT TTTATAAGTA TTTACTATCAA CCTCCGAACC ATCCAAATTC TTATCAAAAA	sspI
668	A S L W N W F S I T K W L W Y I K I F I M I V G G L V G L R I V F	
		^ 43f6, forward
		^ 2000, reverse
2101	GCTGTACTTT CTATAGTGAA TAGAGTTAGG CAGGGATACT CACCATTATC GTTTCAGACC CGCCTCCCAG CCCCAGGAG ACCCGACAGG CCCGAAGGAA	scfI avaI bsaI

TABLE 2-continued

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CGACAATGAAA GATATCACTT ATCTCAATCC GTCCCTATGA GTGTAATAG CAAAGTCTGG GCGGAGGTC GGGGCTCCTC TGGGCTGTCC GGGCTTCCTT
701 A V L S I V N R V R Q G Y S P L S F Q T R L P A P R R P D R P E G I

                                xcmI
                                bstYI/xhoII
                                earI/ksp632I
                                eco57I
2201 TCGAAGAAGA AGGTGGAGAG CAAGGCAGAG ACAGATCCAT TCGCTTAGTG GATGGATTCT TAGCACTTAT CTGGGACGAC CTACGGAGCC TGTGCCCTCTT
AGCTTCTTCT TCCACCTCTC GTTCCGCTCT TGTCTAGGTA AGCGAATCAC CTACCTAAGA ATCGTGAATA GACCTTGCTG GATGCCCTCGG ACACGGAGAA
735 E E E G G E Q G R D R S I R L V D G F L A L I W D D L R S L C L F

                                ^
                                r1,reverse

2301 CAGCTACCAC CGCTTGAGAG ACTTACTCTT GATTGCAACG AGGATTGTGG AACTTCTGGG ACGCAGGGGG TGGGAAGCCC TCAAAATATTG GTGGAATCTC
GTCGATGGTG GCGAACTCTC TGAATGAGAA CTAACGTTGC TCCTAACACC TTGAAGACCC TCGGTCCCCC ACCCTTCGGG AGTTATAAC CACCTTAGAG
768 S Y H R L R D L L L I A T R I V E L L G R R G W E A L K Y W W N L

                                sspI

                                alwNI
                                scfI
2401 CTACAGTATT GGATTGAGG ACTAAAGAAT AGTGTGTTA GCTTGCTTAA TGTACAGCC ATAGCAGTAG CTGAGGGGAC AGATAGGGTT TTAGAAGTAT
GATGTCATAA CCTAAGTCTT TGATTTCTTA TCACGACAAT CGAACGAATT ACAGTGTGCG TATCGTCATC GACTCCCTG TCTATCCCAA AATCTTCATA
801 L Q Y W I Q E L K N S A V S L L N V T A I A V A E G T D R V L E V L

                                alwNI
                                scfI
2501 TACAAAGAGC TTATAGAGCT ATTCTCCACA TACCTACAAG AATAAGACAG GGCCTTGAAA GGGCTTTGCT ATAA
ATGTTTCTCG AATATCTCGA TAAGAGGTGT ATGGATGTTT TTTATTTCTG CCGAACCTTT CCCGAAACGA TATT
835 Q R A Y R A I L H I P T R I R Q G L E R A L L O

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hgICl      scfI
banI      pstI
bsp1286   bsgI
bmyI      scfI
          styI
1 ATGAGACTGA AGAGGATCAG GAGGAATTAT CAGCACTTGT GAAAATGGG CACCATGCTC CTGGGATGT TGATGATCTG TAGTGTCTGA GAAAAATTGT
TACTTCACT TCTCCTAGTC CTCCTTAATA GTCGTGAACA CCTTTACCC GTGGTACGAG GAACCCCTACA ACTACTAGAC ATCAGGACGT CCTTTTAAACA
1 M R V K R I R R N Y Q H L W K W G T M L L G M L M I C S A A G K L W

kpnI
hgICl
banI
asp718
acc65I
101 GGTGCACAGT CTATTATGGG GTACCTGTGT GAAAAGAAAC AACCCACACT CTATTTTGTG CATCAGATGC TAAAGCATAT GATACAGAGA TACATAATGT
CCCAGTCTCA GATAATACCC CATGGACACA CCTTCTTTTG TTGGTGGTGA GATAAAACAC GTAGTCTACG ATTTCCGTATA CTATGTCTCT ATGTAATTACA
35 V T V Y Y G V P V W K E T T T T L F C A S D A K A Y D T E I H N V

nspI      nspI
nspHI     nspHI
          apoI      ahlII
201 TTGGGCCACA CATGCCCTGT TACCCACAGA CCCCACCCCA CAAGAAGTAG TATTGAAAAA TGTGACAGAA AATTTTAAACA TGTGGAAAAA TAACATGGTG
AACCCGGTGT GTACGGACAC ATGGGTGTCT GGGGTGGGT GTTCTTCATC ATAACCTTTT ACACGTCTT TTAATAATTGT ACACCTTTT ATTTGACCAC
68 W A T H A C V P T D P N P Q E V V L E N V T E N F N M W K N N M V

ppu10I
nsII/avaIII
          draIII
          ahaIII/draI
301 GAACAGATGC ATGAGGATAT AATCAGTTTA TGGGATCAAA GTCTAAAGCC ATGTGTAAAA TTAACCCAC TCTGTGTAC TTTAAATTGC ACTGATGCCG
CTTGTCTACG TACTCCTATA TTAGTCAAT ACCCTAGTTT CAGATTTCGG TACACATTTT AATTGGGGTG AGACACATG AATTTTAAACG TGACTACGCC
101 E Q M H E D I I S L L W D Q S L K P C V K L T P L C V T L N C T D A G

gsuI/bpmI
401 GGAATACTAC TAATACCAAT AGTAGTAGC GGGAAAAGCT GGAGAAAGGA GAAATAAAAA ACTGCTCTT CAATATCACC ACAAGCATGA GAGATAAGAT
CCTTATGATG ATTATGGTTA TCATCATCGC CCTTTTTCGA CCTTTTTCCT CTTTATTTT TGACGAGAAA GTTATAGTGG TGTTCGTACT CTCTATTCTA
135 N T T N T N S S S G E K L E K G E I K N C S F N I T T S M R D K M

scaI      scaI      scfI
501 GCAGAGAGAA ACTGCACCTT TTAATAAACT TGATATAGTA CCAATAGATG ATGATGATAG GAATAGTACT AGGAATAGTA CTAACATATAG GTTGATAAGT
CGTCTCTCTT TGACGTGAAA AATTAATTTGA ACTATATCAT GGTATATCTAC TACTACTATC CTTATCATGA TCCTTATCAT GATTGATATC CAACATATCA
168 Q R E T A L F N K L D I V P I D D D R N S T R N S T N Y R L I S

stul
haeI
601 TGTAACACCT CAGTCATTAC ACAGGCCTGT CCAAAGGTAT CATTGAGCC AATCCCATTA CATTCTGTA CCCCCTGGT TTTTGGCTT CTAAGTGTGA
ACATTGTGGA GTCAGTAAAG TGTCCGGACA GGTTCCTATA GTAACCTCGG TTAAGGTAT GTAAGACAT GGGCCCGACC AAAACCGGAA GATTTACAT
201 C N T S V I T Q A C P K V S F E P I P I H F C T P A G F A L L K C N

scaI      bsp1407I      haeI
701 ATAAAGAGAC GTTCAATGGA TCAGGACCAT GCAAAAATGT CAGCACAGTA CTATGTACAC ATGGAATTAG GCCAGTAGTA TCAACTCAAC TGTGTTAAA
TATTACTCTG CAAGTTACCT AGTCCCTGGTA CGTTTTTACA GTCGTGTCTAT GATACATGTG TACCTTAATC CCGTCACTAT AGTTGAGTTG ACGACAATTT
235 N E T F N G S G P C K N V S T V L C T H G I R P V V S T Q L L N

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801 TGGCAGTCTA GCAGGAGAAG AGGTAGTAAAT TAGATCTGAA AATTTCCAGG ACAATGCTAA AACATAATA GATACAGCTCA AAGAACCAGT AAAAAATTAAT
    earI/ksp632I          bstYI/xhoII          bglII apoI          aseI/asnI/vspI
ACCCTCAGAT CGTCCCTCTC TCCATCATTA ATCTAGACTT TAAAGTGT TTAAGTGT CATGTCGAGT TTCCTGGTCA TTTTAAATTA
268 G S L A G E V I R S E N F T N A K T I I V Q L K E P V K I N
    bst1107I
    accI scfI
901 TGTACAAGAC CCAACAACAA TACAAGAAA AGTATACCTA TAGGACCAGG GAGAGCATTT TATGCAACAG GCGACATAAT AGGAAATATA AGACAAGCAC
    bspI407I          TCAATGTTCTG GGTGTTGTTT ATGTTCTTTT TCAATATGGAT ATCCTGGTCC CTCCTGTAATA TCCTTTATAT TCTGTTCCGTG
301 C T R P N N N T R K S I P I G P G R A F Y A T G D I I G N I R Q A H
    eeo81I
    bsu36I/mstII/sauI
1001 AATTGTAACCT TAGTAGAACA GACTGGAATA ACACTTTAAG ACAGATAGCT GAAAAATTA GAAAAAATTT TGGGAATAAA ACAATAATCT TTAATCACTC
    TAAACAATTGGA ATCATCTTGT CTGACCTTAT TGTGAAATTC TGTCTATCGA CTTTAAATTT TGTGTAATA ACCCTTATTT TGTATATAGA AATTAGTGAG
335 C N L S R T D W N N T L R Q I A E K L R K Q F G N K T I I F N H S
    ppuMI
    eeo0109I/draII
1101 CTCAGGAGGG GACCCAGAAA TTGTAATGCA CAGTTTAAAT TGTAGAGGGG AATTTTCTA CTGTGATACA ACACAATTTGT TTAACAGTAC TTGGAATGCA
    GAGTCCCTCC CTGGGTCTTT AACATTTACGT GTCAAAATTA ACATCTCCCC TAAAAAAGAT GACACTATGT TGTGTTAACA AATGTGTCAT AACCTTACGT
368 S G G D P E I V M H S F N C R G E F F Y C D T T Q L F N S T W N A
    nspI
    nsPHI
    aflIII
1201 AATAACACTG AAAGGAATAG CACTAAAGAG AATAGCACAA TCACACTCCC ATGCAGAA TAACAAAATTTG TAAACATGCG GCAGGAAGTA GGAATAAGCAA
    TTAATTGTGAC TTTCCTTATC GTGATTTCTC TTATCGTGT AGTGTGAGG TACGCTTAT TTTGTTTAAAC AATTTGTACAC CGTCTTCAT CCTTTTCCGTT
401 N N T E R N S T K E N S T I T L P C R I K Q I V N M W Q E V G K A M
    memI
    bsaBI
    sspI
1301 TGTATGCCCC TCCCATCAGA GGACAAAATA GATGTTTATC AATATTACA GGGTTGCTAT TAACAAGAGA TGGAGGTAGT AGCAACAGCA TGAATGAGAC
    ACAATACGGGG AGGGTAGTCT CCTGTTTAAAT CTACAAGTAG TTTATAAATGT CCCAACGATA ATGTTCTCT ACCTCCATCA TCGTTGTCGT ACTTACTCTG
435 Y A P P I R G Q I R C S S N I T G L L L T R D G G S S N S M N E T
    gsuI/bpmI
    munI
    styI
1401 CTTACAGACT GGAGGAGGAG ATATGAGGGA CAATTGGAGA AGTGAATTTAT ACAATAATAA AGTAGTAAA ATTGAACCAT TAGGAGTAGC ACCCACCAAG
    GAAGTCTGGA CCTCCTCCTC TATACTCCCT GTTAAACCTCT TCACITTAATA TGTTTATATT TCATCATTTT TAACITGGTA ATCCTCATCG TGGGTGGTTC
468 F R P G G G D M R D N W R S E L Y K Y K V V K I E P L G V A P T K
    earI/ksp632I
    styI
1501 GCAATGAGAA GAGTGGTGCA GAGAGAAA AAAGCAGTGG GAATAGGAGC TGTGTTCTCT TGGTCTTAG GAGCAGCAGG AAGCACTATG GCGCAGCGGT
    CGTTACTCTT CTCACCACGT CTCTCTTTT TCTCGTCACT CTTATCCTCG ACACAAGGAA CCCAAGAATC CTCGTGCTCC TTCGTGATAC CCGCGTCCGCA
501 A M R R V V Q R E K R A V G I G A V F L G F L G A A G S T M G A A S
    haeI
    alwNI
1601 CAATAACGCT GACGGTACAG CCGGACTAT TATTGCTGG TATAGTGCAA CAGCAGAA CAATTTGCTG GGCATTTGAG GCGCAACAGC ATCTGTTGCA
    GTTATTGCGA CTGCCATGTC CCGTCTGATA ATAACAGACC ATATCACGTT GTCGTTGT TAAACGACTC CCGATAACTC CGCGTTGTCG TAGACAACGT
535 I T L T V Q A R L L L S G I V Q Q N N L L R A I E A Q Q H L L Q

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          gsuI/bpmI          eco81I          alwNI
          bsu36I/mstII/sauI
1701 ACTCACAGTC TGGGGCATCA AGCAGCTCCA GCGAAGAGTC CTGGCTGTGG AAGATACCT AAGGGATCAA CAGCTCCTGG GGATTTGGGG TTGCTCTGGA
    TGAGTGTGAG ACCCGTAGT TCGTGGAGGT CCGTTCAG GACCGACACC TTTCTATGGA TTCCCTAGTT GTCGAGGACC CCTAAACCCC AACGAGACCT
568 L T V W G I K Q L Q A R V L A V E R Y L R D Q Q L L G I W G C S G

          styI bsmI          xbaI
          hindIII
1801 AAATCAATTT GCACCACCTC TGTGCCTTGG AATGCTAGTT GGAGTAATAA ATCTCTAGAT AAGATTTGGG ATAACATGAC CTGGATGGAG TGGGAAAGAG
    TTTGAGTAAA CGTGGTGGAG ACACGGAAAC TTACGATCAA CCTCAATTTT TAGAGATCTA TTCTAAACCC TATTGTACTG GACCTACCTC ACCCTTTCTC
601 K L I C T T S V P W N A S W S N K S L D K I W D N M T W M E W E R E

          hindIII
1901 AAATTGAGAA TTACACAAGC TTAATATACA CCTTAANTGA AGAATCGCAG AACCAACAAG AAAAGAATAA ACAAGACTTA TTGGAATTGG ATCAATAGGC
    TTTAACTCTT AATGTGTTGG AATTAATATGT GGAATTAAGT TCTTAGCGTC TTGTTGTTTC TTTTCTTATT TGTTCCTGAT AACCTTAACC TAGTTATCCG
635 I E N Y T S L I Y T L I E E S Q N Q Q E K N K Q D L L E L D Q O A

          sspI
2001 AAGTTTGTGG AATTGGTTTA GCATAACAAA ATGGCTGTGG TATATAAAA TATTCATAAT GATAGTTGGA GGCITGGTAG GTTTAAGAAT AGTTTTTGGT
    TTCAAACACC TTAACCAAAT CGTATTGTTT TACCGACACC ATATATTTTT ATAGTATTA CTATCAACCT CCGAACCATC CAAATCTTA TCAAAAACGA
668 S L W N W F S I T K W L W Y I K I F I M I V G G L V G L R I V F A

          scfI          ppuMI          eco57I          earI/ksp632I
          bstYI/xhoII
2101 GTACTTTCTA TAGTGAATAG AGTTAGGCAG GGTACTACAC CATTATCATT TCAGACCCGC CTCCCAGCCC CGAGGGGACC CGACAGGCC AAAGGAATCG
    CATGAAAGAT ATCACTTATC TCAATCCGTC CCCATGAGTG GTAATAGTAA AGTCTGGCG GAGGTCCGG GCTCCCTGG GCTGTCCGGG TTTCCCTTAGC
701 V L S I V N R V R Q G Y S P L S F Q T R L P A P R G P D R P K G I E

          xcmI
          sspI
2201 AAGAGAAGG TGGAGAGCAA GACAGGGACA GATCCATTCG CTTAGTGGAT GGAFTCTTAG CACTTATCTG GGACGATCTA CGGAGCCTGT GCCTCTTCAG
    TTTCTTCTCC ACCTCTCGTT CTGTCCCTGT CTAGGTAAGC GAATCACCTA CCTAAGAATC GTGAATAGAC CCTGCTAGAT GCCTCGGACA CGGAGAAGTC
735 E E G G E Q D R D R S I R L V D G F L A L I W D D L R S L C L F S

          sspI          scfI
2301 CTACACCCGC TTGAGAGACT TACTCTTGAT TGC AACGAGG ATTGTGGAAC TTCTGGGACG CAGGGGGTGG GAAGCCCTCA AATATGGTG GAATCTCCTA
    GATGTTGGCG AACTCTCTGA ATGAGAACTA ACGTTGCTCC TAACACCTTG AAGACCTTG GTCCCCACC CCTTCGGAGT TTATAACCCAC CTTAGAGGAT
768 Y H R L R D L L L I A T R I V E L L G R R G W E A L K Y W W N L L

          alwNI          xbaI
2401 CAGTATTGGA TTCAGGAAC TTAAGAATAGT GCTGTTAGCT TGTTAATGT CACAGCCATA GCAGTAGCTG AGGGGACAGA TAGGGTTCTA GAAGCATTCG
    GTCATAACCT AAGTCCCTGA TTTCTTTATCA CGACAATCGA ACGAATTACA GTGTCCGTAT GTCCCTGTCT ATCCCAAGAT CTTCGTAACG
801 Q Y W I Q E L K N S A V S L L N V T A I A V A E G T D R V L E A L Q

          alwNI
2501 AAAGAGCTTA TAGAGCTATT CTCCACATAC CTACAAGAAT AAGACAAGGC TTGAAAGGG CTTTGTATATA A
    TTTCTCGAAT ATCTCGATAA GAGGTGTATG GATGTTCTTA TTCTGTCCG AACCTTCCC GAAACGATAT T
835 R A Y R A I L H I P T R I R Q G L E R A L L O

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length: 2571

Table 3 illustrates the amino acid sequences for the GNE₈ and different GNE₁₆ gp120 proteins. The regions of the sequences having identical amino acid sequences are

enclosed in boxes. Note: the "X" in position 666 of sequence gp160.SF.16.7 is a stop codon.

TABLE 3

gp160.8.24	1	MIVKGI RKN C QHLWRWG TMLLGM L MICSAAE K LWVT VYYGVPVWKEA TTT
gp160.SF.16.2	1	MRVKG IRRNY QHLWRWG TMLLGI L MICSAA G KLWVT VYYGVPVWKE TTT
gp160.SF.16.7	1	MRVKR IRRNY QHLWK WG TMLLGM L MICSAA G KLWVT VYYGVPVWKE TTT
gp160.8.24	51	LFCASDAKAYDTEV HNVWATHACVPTDPNPQE I G LENVTFENFNMWKNM V
gp160.SF.16.2	51	LFCASDAKAYDTEI HNVWATHACVPTDPNPQE V V LENVTFENFNMWKNM V
gp160.SF.16.7	51	LFCASDAKAYDTEI HNVWATHACVPTDPNPQE V V LENVTFENFNMWKNM V
gp160.8.24	101	EQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDL KNA T N T T S S S W G K M E R G
gp160.SF.16.2	101	EQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDAGN T T N T N S S S R E K L E K G
gp160.SF.16.7	101	EQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDAGN T T N T N S S S G E K L E K G
gp160.8.24	151	EIKNC SFN V T T S I RDKM K N E Y A L F Y K L D V V P I D N D N T S Y R L I S
gp160.SF.16.2	151	EIKNC SFN I T T S V RDKM Q K E T A L F N K L D I V P I D D D D R N S T R N S T N Y R L I S
gp160.SF.16.7	151	EIKNC SFN I T T S M RDKM Q R E T A L F N K L D I V P I D D D D R N S T R N S T N Y R L I S
gp160.8.24	194	CNTSVITQACP KVSFEPIPIHY C A P A G F A I L K C R D K K F N G T G P C T N V S T V
gp160.SF.16.2	201	CNTSVITQACP KVSFEPIPIHF C T P A G F A L L K C N N K T F N G S G P C K N V S T V
gp160.SF.16.7	201	CNTSVITQACP KVSFEPIPIHF C T P A G F A L L K C N N E T F N G S G P C K N V S T V
gp160.8.24	244	QCTHGIRPVVSTQ LLLNGSLAE E E V V I R S A N F S D N A K T I I V Q L N E S V E I N
gp160.SF.16.2	251	QCTHGIRPVVSTQ LLLNGSLAE G E V V I R S E N F T N N A K T I I V Q L T E P V K I N
gp160.SF.16.7	251	LCTHGIRPVVSTQ LLLNGSLA G E V V I R S E N F T N N A K T I I V Q L K E P V K I N
gp160.8.24	294	CTRPNNNTR R S I H I G P G R A F Y A T G E I I G D I R Q A H C N L S S T K W N N T L K Q I V
gp160.SF.16.2	301	CTRPNNNTR K S I P I G P G R A F Y A T G D I I G N I R Q A H C N L S R T D W N N T L G Q I V
gp160.SF.16.7	301	CTRPNNNTR K S I P I G P G R A F Y A T G D I I G N I R Q A H C N L S R T D W N N T L R Q I A
gp160.8.24	344	TKLREHF . N K T I V F N H S S G D P E I V M H S F N C R G E F F Y C N T T P L F N S T W N Y
gp160.SF.16.2	351	EKLREQFG N K T I I F N H S S G D P E I V M H S F N C R G E F F Y C N T T Q L F D S T W D N
gp160.SF.16.7	351	EKLRLKQFG N K T I I F N H S S G D P E I V M H S F N C R G E F F Y C D T T Q L F N S T W N A
gp160.8.24	393	TYTWNTEG S N D T G R N I T L Q C R I K Q I I N M W Q E V G K A M Y A P P I R G Q I R C S S
gp160.SF.16.2	401	TKV . . S N G T S T E E N S T I T L P C R I K Q I V N M W Q E V G K A M Y A P P I R G Q I R C S S
gp160.SF.16.7	401	NNT . . E R . N S T K E N S T I T L P C R I K Q I V N M W Q E V G K A M Y A P P I R G Q I R C S S
gp160.8.24	443	NITGLLLTRDGG . N N S E T E I F R P G G G D M R D N W R S E L Y K Y K V V K I E P L G V A
gp160.SF.16.2	449	NITGLLLTRDGG S N N S M N E T F R P G G G D M R D N W R S E L Y K Y K V V K I E P L G V A
gp160.SF.16.7	448	NITGLLLTRDGG S S N S M N E T F R P G G G D M R D N W R S E L Y K Y K V V K I E P L G V A
gp160.8.24	492	PTKAK RRV M Q R E K R A V G I G A V F L G F L G A A G S T M G A A S V T L T V Q A R L L L S G
gp160.SF.16.2	499	PTKAK RRV V Q R E K R A V G I G A V F L G F L G A A G S T M G A A S I T L T V Q A R L L L S G
gp160.SF.16.7	498	PTKAM RRV V Q R E K R A V G I G A V F L G F L G A A G S T M G A A S I T L T V Q A R L L L S G
gp160.8.24	542	IVQQQNNLLRAIEAE Q H L L Q L T V W G I K Q L Q A R V L A V E R Y L K D Q Q L L G I W G
gp160.SF.16.2	549	IVQQQNNLLRAIEAQ Q H L L Q L I V W G I K Q L Q A R V L A V E R Y L R D Q Q L L G I W G
gp160.SF.16.7	548	IVQQQNNLLRAIEAQ Q H L L Q L T V W G I K Q L Q A R V L A V E R Y L R D Q Q L L G I W G
gp160.8.24	592	CSGKLICTT A V P W N A S W S N K S L D K I W D N M T W M E W E R E I D N Y T S L I Y S L I E
gp160.SF.16.2	599	CSGKLICTT S V P W N A S W S N K S L D K I W D N M T W M E W E R E I E N Y T S L I Y T L I E
gp160.SF.16.7	598	CSGKLICTT S V P W N A S W S N K S L D K I W D N M T W M E W E R E I E N Y T S L I Y T L I E
gp160.8.24	642	ESQNQQEKNE Q E L L E L D K W A S L W N W F D I T K W L W Y I K I F I M I V G G L V G L R I
gp160.SF.16.2	649	ESQNQQEKNE Q D L L E L D Q W A S L W N W F S I T K W L W Y I K I F I M I V G G L V G L R I
gp160.SF.16.7	648	ESQNQQEKNE Q D L L E L D Q X A S L W N W F S I T K W L W Y I K I F I M I V G G L V G L R I
gp160.8.24	692	VFT VLSIVNRVRK GYSPLSFQTHLPAPRGLDRPEGT EEEGGERDRDRSSR
gp160.SF.16.2	699	VFAVLSIVNRVRQ GYSPLSFQTRLPAPRRPDRPEGEIEEEEGGEQGRDRSIR
gp160.SF.16.7	698	VFAVLSIVNRVRQ GYSPLSFQTRLPAPRGPDRPKGI EEEEGGEQDRDRSIR
gp160.8.24	742	LVDGFLAIVWV DLRSLCLFSYHRLRDLLLIAA RIVELLGRRGW EALKYWW
gp160.SF.16.2	749	LVDGFLALIWD DLRSLCLFSYHRLRDLLLIAT RIVELLGRRGW EALKYWW
gp160.SF.16.7	748	LVDGFLALIWD DLRSLCLFSYHRLRDLLLIAT RIVELLGRRGW EALKYWW

TABLE 3-continued

gp160.8.24	792	NLLQYWIQELKNSAVSLLN	ATAI	VAE	GTDRV	I	E	I	V	Q	R	A	R	A	I	L	H	I	P	T	R	I	
gp160.SF.16.2	799	NLLQYWIQELKNSAVSLLN	V	TAI	VAE	GTDRV	L	E	V	L	Q	R	A	R	A	I	L	H	I	P	T	R	I
gp160.SF.16.7	798	NLLQYWIQELKNSAVSLLN	V	TAI	VAE	GTDRV	L	E	A	L	Q	R	A	R	A	I	L	H	I	P	T	R	I
gp160.8.24	842	RQGLERALL																					
gp160.SF.16.2	849	RQGLERALL																					
gp160.SF.16.7	848	RQGLERALL																					

Nucleic acid sequences encoding gp120 from GNE₈ and GNE₁₆ capable of expressing gp120 can be prepared by conventional means. The nucleotide sequence can be synthesized. Alternatively, another HIV nucleic acid sequence encoding gp120 can be used as a backbone and altered at any differing residues by site directed mutagenesis as described in detail in Example 1.

In a preferred embodiment, the nucleotide sequence is present in an expression construct containing DNA encoding gp120 under the transcriptional and translational control of a promoter for expression of the encoded protein. The promoter can be a eukaryotic promoter for expression in a mammalian cell. In cases where one wishes to expand the promoter or produce gp120 in a prokaryotic host, the promoter can be a prokaryotic promoter. Usually a strong promoter is employed to provide high level transcription and expression.

The expression construct can be part of a vector capable of stable extrachromosomal maintenance in an appropriate cellular host or may be integrated into host genomes. Normally, markers are provided with the expression construct which allow for selection of a host containing the construct. The marker can be on the same or a different DNA molecule, desirably, the same DNA molecule.

The expression construct can be joined to a replication system recognized by the intended host cell. Various replication systems include viral replication systems such as retroviruses, simian virus, bovine papilloma virus, or the like. In addition, the construct may be joined to an amplifiable gene, e.g. DHFR gene, so that multiple copies of the gp120 DNA can be made. Introduction of the construct into the host will vary depending on the construct and can be achieved by any convenient means. A wide variety of prokaryotic and eukaryotic hosts can be employed for expression of the proteins.

Preferably, the gp120 is expressed in mammalian cells that provide the same glycosylation and disulfide bonds as in native gp120. Expression of gp120 and fragments of gp120 in mammalian cells as fusion proteins incorporating N-terminal sequences of Herpes Simplex Virus Type 1 (HSV-1) glycoprotein D (gD-1) is described in Lasky, L. A. et al., 1986 (Neutralization of the AIDS retrovirus by antibodies to a recombinant envelope glycoprotein) *Science* 233: 209-212 and Haffar, O. K. et al., 1991 (The cytoplasmic tail of HIV-1 gp160 contains regions that associate with cellular membranes.) *Virology* 180:439-441, respectively. A preferred method for expressing gp120 is described in Example 3. In the example, a heterologous signal sequence was used for convenient expression of the protein. However, the protein can also be expressed using the native signal sequence.

An isolated, purified GNE₈-gp120 and GNE₁₆-gp120 having the amino acid sequence illustrated in Tables 1-3 can be produced by conventional methods. For example, the proteins can be chemically synthesized. In a preferred

embodiment, the proteins are expressed in mammalian cells using an expression construct of this invention. The expressed proteins can be purified by conventional means. A preferred purification procedure is described in Example 3. gp120 Fragments

The present invention also provides gp120 fragments that are suitable for use in inducing antibodies for use in serotyping or in a vaccine formulation. A truncated gp120 sequence as used herein is a fragment of gp120 that is free from a portion of the intact gp120 sequence beginning at either the amino or carboxy terminus of gp120. A truncated gp120 sequence of this invention is free from the C5 domain. The C5 domain of gp120 is a major immunogenic site of the molecule. However, antibodies to the region do not neutralize virus. Therefore, elimination of this portion of gp120 from immunogens used to induce antibodies for serotyping is advantageous.

In another embodiment, the truncated gp120 sequence is additionally free from the carboxy terminus region through about amino acid residue 453 of the gp120 V5 domain. The portion of the V5 domain remaining in the sequence provides a convenient restriction site for preparation of expression constructs. However, a truncated gp120 sequence that is free from the entire gp120 V5 domain is also suitable for use in inducing antibodies.

In addition, portions of the amino terminus of gp120 can also be eliminated from the truncated gp120 sequence. The truncated gp120 sequence can additionally be free from the gp120 signal sequence. The truncated gp120 sequence can be free from the amino terminus through amino acid residue 111 of the gp120 C1 domain, eliminating most of the C1 domain but preserving a convenient restriction site. However, the portion of the C1 domain through the cysteine residue that forms a disulfide bond can additionally be removed, so that the truncated gp120 sequence is free from the amino terminus through amino acid residue 117 of the gp120 C1 domain. Alternatively, the truncated gp120 sequence can be free from the amino terminus of gp120 through residue 111 of the C1 domain, preserving the V2 disulfide bond. In a preferred embodiment, the truncated gp120 sequence is free from the amino terminus of gp120 through residue 111 of the C1 domain and residue 453 through the carboxy terminus of gp120.

The truncated gp120 sequences can be produced by recombinant engineering, as described previously. Conveniently, DNA encoding the truncated gp120 sequence is joined to a heterologous DNA sequence encoding a signal sequence.

Serotyping Method

The present invention also provides an improved serotyping method for HIV strains. The method comprises determining the serotypes of the V2, V3, and C4 domains of gp120.

HIV isolates can be serotyped by conventional immunoassay methods employing antibodies to the neutralizing

epitopes in the V2, V3, and C4 domains for various strains of HIV. Preparation of the antibodies is described hereinbefore. The antibody affinity required for serotyping HIV using a particular immunoassay method does not differ from that required to detect other polypeptide analytes. The antibody composition can be polyclonal or monoclonal, preferably monoclonal.

A number of different types of immunoassays are well known using a variety of protocols and labels. The assay conditions and reagents may be any of a variety found in the prior art. The assay may be heterogeneous or homogeneous. Conveniently, an HIV isolate is adsorbed to a solid phase and detected with antibody specific for one strain of neutralizing epitope for each neutralizing epitope in the V2, V3, and C4 domain. Alternatively, supernatant or lysate from the cultured isolate which contains gp120 can be adsorbed to the solid phase. The virus or gp120 can be adsorbed by many well known non-specific binding methods. Alternatively, an anti-gp120 antibody, preferably directed to the carboxy terminus of gp120 can be used to affix gp120 to the solid phase. A gp120 capture antibody and sandwich ELISA assay for gp120 neutralizing epitopes is described by Moore, *AIDS Res. Hum. Retroviruses* 9:209–219 (1993). Binding between the antibodies and sample can be determined in a number of ways. Complex formation can be determined by use of soluble antibodies specific for the anti-gp120 antibody. The soluble antibodies can be labeled directly or can be detected using labeled second antibodies specific for the species of the soluble antibodies. Various labels include radionuclides, enzymes, fluorescers, colloidal metals or the like. Conveniently, the anti-gp120 antibodies will be labeled directly, conveniently with an enzyme.

Alternatively, other methods for determining the neutralizing epitopes can be used. For example, fluorescent-labeled antibodies for a neutralizing epitope can be combined with cells infected by the strain of HIV to be serotyped and analyzed by fluorescence activated cell sorting.

The serotype of the HIV isolate includes the strain of the neutralizing epitopes for the V2, V3, and C4 domains.

It is understood that the application of the teachings of the present invention to a specific problem or situation will be within the capabilities of one having ordinary skill in the art in light of the teachings contained herein. Examples of the products of the present invention and representative processes for their isolation, use, and manufacture appear below, but should not be construed to limit the invention. All literature citations herein are expressly incorporated by reference.

EXAMPLE 1

Identification of C4 Neutralizing Epitopes

The following reagents and methods were used in the studies described herein.

gp120 Sequences and Nomenclature

Amino acid residues are designated using the standard single letter code. The location of amino acids within the gp120 protein is specified using the initiator methionine residue as position 1. The designation LAI is used to describe the virus isolate from which the HIV-1_{BH10}, HIV-1_{IIIB}, HIV-1_{BRU}, HIV-1_{HXB2}, HIV-1_{HXB3} and HIV-1_{HXB10} substrains (molecular clones) of HIV-1 were obtained. The sequence of gp120 from IIIB substrain of HIV-1_{LAI} is that determined by Muesing et al. (30).

The sequence of gp120 from MN strain of HIV-1 is given with reference to the MNgp120 clone (MN_{GNE}). The sequence of this clone differs by approximately 2% from that

of the MN₁₉₈₄ clone described by Gurgo et al. (13). The sequences of gp120 from the NY-5, JRcsf, Z6, Z321, and HXB2 strains of HIV-1 are those listed by Myers et al. (32) except where noted otherwise. The sequence of the Thai isolate A244 is that provided by McCutchan et al. (24). The variable (V) domains and conserved (C) domains of gp120 are specified according to the nomenclature of Modrow et al. (28).

Monoclonal Antibody Production and Screening Assays

Hybridomas producing monoclonal antibodies to MN-rgp120 (recombinantly produced gp120 from the MN strain of HIV) (3) were prepared and screened for CD4 blocking activity as described previously (7, 33). The binding of monoclonal antibodies to MN-rgp120 and to rgp120s from the IIIB, NY-5, Z6, Z321, JRcsf, and A244 strains of HIV-1 was assessed by enzyme linked immunoadsorbant assays (ELISA) as described previously (33).

Virus Binding and Neutralization Assays

The ability of monoclonal antibodies to neutralize HIV-1 infectivity in vitro was assessed in a colorimetric MT-2 cell cytotoxicity assay similar to that described previously (35). MT-2 cells and H9/HTLV-III_{MN} cells were obtained through the AIDS Research and Reference Reagent Program, Division of AIDS, NIAID, NIH: contributed by Drs. Douglas Richman and Robert Gallo, respectively. Briefly, serial dilutions of antibody or serum were prepared in 50 μ l volumes of complete and then 50 μ l of a prediluted HIV-1 stock was added to each well. After incubation for 1 hr at 4° C., 100 μ l of a 4 \times 10⁵ MT-2 cell/ml suspension was added. After incubation of the plates for 5 days at 37° C. in 5% CO₂, viable cells were measured using metabolic conversion of the formazan MTT dye. Each well received 20 μ l of a 5 mg/ml MTT solution in PBS.

After a 4 hr incubation at 37° C., the dye precipitate was dissolved by removing 100 μ l of the cell supernatant, adding 130 μ l of 10% Triton X-100 in acid isopropanol, then pipeting until the precipitate was dissolved. The optical density of the wells was determined at 540 nm. The percentage inhibition was calculated using the formula:

$$\frac{1 - (\text{virus control} - \text{experimental})}{(\text{virus control} - \text{medium control})}$$

Cell Surface Staining of HIV-1 Infected Cells with Monoclonal Antibodies

H9 cells (2 \times 10⁵) chronically infected with the IIIB, HXB2, HXB3, and HX10 substrains of HIV-1_{LAI} or with HIV-1_{MN} were incubated for 30 min at room temperature with monoclonal antibodies (10 μ g per ml) in 100 μ l of RPMI 1640 cell culture media containing 1% FCS. Cells were washed and then incubated with 20 μ g per ml of fluorescein-conjugated, affinity-purified, goat antibody to mouse IgG (Fab')₂ (Cappel, West Chester, Pa.) for 30 min. Cells were washed, fixed with 1% paraformaldehyde and the bound antibody was quantitated by flow cytometry using a FACSCAN (Becton-Dickenson, Fullerton, Calif.).

Fluorescence data was expressed as percentage of fluorescent cells compared to the fluorescence obtained with the second antibody alone. Fluorescence was measured as the mean intensity of the cells expressed as mean channel number plotted on a log scale.

Fragmentation of the MN-rgp120 Gene

Fragments of the MN-rgp120 gene were generated using the polymerase chain reaction (PCR) (17). Briefly, forward 30-mer oligonucleotide DNA primers incorporating a Xho I site, and reverse 36-mer oligonucleotide DNA primers con-

taining a stop codon followed by a Xba 1 site were synthesized and used for the polymerase chain reactions. Thirty cycles of the PCR reaction were performed using 0.3 μ g of a plasmid containing the gene for gp120 from the MN strain of HIV-1 (pRKMN. D533) and 0.04 nM of a designated primers. The PCR reaction buffer consisted of 0.1 M Tris buffer (pH 8.4), 50 mM KCl, 0.2 mM 4dNTP (Pharmacia, Piscataway, N.J.), 0.15 M MgCl₂ and 0.5 Unit of Taq Polymerase (Perkin-Elmer Cetus, Norwalk, Conn.) and a typical PCR cycle consisted of a 60 second denaturation step at 94° C., followed by a 45 second annealing step at 55° C., and then an extension step at 72° C. for 45 seconds.

Following the PCR amplification, the PCR products were purified by phenol and chloroform extraction, and then ethanol precipitated. The purified products were then digested with the restriction endonucleases Xho1 and Xba1. The resulting PCR products were gel purified using 1% agarose (SEAKEM, FMC Bioproducts, Rockland, Me.) or 5% polyacrylamide gel electrophoresis (PAGE) and then isolated by electroelution.

Site Directed Mutagenesis of the MN-rgp120 C4 Domain

A recombinant PCR technique (15) was utilized to introduce single amino acid substitutions at selected sites into a 600 bp Bgl II fragment of MN-rgp120 that contained the C4 domain. This method entailed the PCR amplification of overlapping regions of the C4 domain of gp120 using primers that incorporated the desired nucleotide changes. The resultant PCR products were then annealed and PCR amplified to generate the final product. For these reactions 18-mer "outside" primers encoding the wild type sequence (Bgl II sites) were amplified with 36-mer "inside" primers that contained the alanine or glutamic acid residue changes. The first PCR reaction included 1 \times of the Vent polymerase buffer (New England Biolabs, Beverly, Mass.), 0.2 mM of 4dNTP (Pharmacia, Piscataway, N.J.), 0.04 nM of each synthetic oligonucleotide, 0.3 μ g of linearized plasmid, pRKMN.D533, which contained the MN-rgp120 gene. Thirty PCR cycles were performed consisting of the following sequence of steps: 45 seconds of denaturation at 94° C., 45 second of annealing at 55° C. and 45 seconds of extension at 72° C. Following PCR amplification, the product pairs were gel purified using a 1% solution of low melt agarose (SeaPlaque, FMC Bioproducts, Rockland, Me.).

The agarose containing PCR product was melted at 65° C. and combined with the PCR product of the overlapping pair and equilibrated to 37° C. Added to this (20 μ l) was 10 μ l of 10 \times Vent Polymerase buffer, 10 μ l of 2 mM 4dNTP, 0.04 nM each of the "outside" wild type 18 mer oligonucleotides, 57 μ l of H₂O and 1 unit of Vent Polymerase. Thirty PCR cycles were performed as previously above.

The resulting PCR products were purified and digested with the Bgl II endonuclease. The digested PCR product was then ligated into the mammalian cell expression vector pRKMN.D533, which had been digested with Bgl II allowing for the removal of a 600 bp fragment. Colonies containing the correct insertion were identified and Sequenase 2.0 supercoil sequencing was employed to check for fidelity and the incorporation of the desired mutation.

Expression of gp120 Fragments in Mammalian Cells

Fragments of the MN and IIIB gp120 were expressed in mammalian cells as fusion proteins incorporating N-terminal sequences of Herpes Simplex Virus Type 1 (HSV-1) glycoprotein D (gD-1) as described previously (14, 22). Briefly, isolated DNA fragments generated by the PCR reaction were ligated into a plasmid (pRK.gD-1) designed to fuse the gp120 fragments, in frame, to the 5' sequences of the glycoprotein D (gD) gene of Type 1 Herpes Simplex Virus

(gD-1) and the 3' end to translational stop codons. The fragment of the gD-1 gene encoded the signal sequence and 25 amino acids of the mature form of HSV-1 protein. To allow for expression in mammalian cells, chimeric genes fragments were cloned into the pRK5 expression plasmid (8) that contained a polylinker with cloning sites and translational stop codons located between a cytomegalovirus promoter and a simian virus 40 virus polyadenylation site.

The resulting plasmids were transfected into the 293s embryonic human kidney cell line (12) using a calcium phosphate technique (11). Growth conditioned cell culture media was collected 48 hr after transfection, and the soluble proteins were detected by ELISA or by specific radioimmuno-precipitation where metabolically labeled proteins from cell culture supernatants were resolved by sodium dodecyl sulfate polyacrylamide gel electrophoresis (PAGE) and visualized by autoradiography as described previously (1, 18). Radioimmunoprecipitation of MN-rgp120 Mutants

Plasmids directing the expression of the MN-rgp120 C4 domain mutants were transfected into 293s cells as described above. Twenty four hours following the transfection, the cells were metabolically labeled with [³⁵S]-labeled methionine or cysteine as described previously (1). The labeled cell culture supernatants were then harvested and 0.5 ml aliquots were reacted with 1–5 μ g of the monoclonal antibody or with 2 μ l of the polyclonal rabbit antisera to MN-rgp120 and immunoprecipitated with Pansorbin (CalBiochem, La Jolla, Calif.) as described previously (1). The resulting Pansorbin complex was pelleted by centrifugation, washed twice with a solution containing PBS, 1% NP-40 and 0.05% SDS and then boiled in a PAGE sample buffer containing 1% 2-mercaptoethanol. The processed samples were analyzed by SDS-PAGE and visualized by autoradiography (1, 18).

Assays to Measure the Binding of Monoclonal Antibodies to Mutagenized MN-rgp120 Polypeptides

An ELISA was developed to screen for reactivity of MN-rgp120 fragments and mutant proteins with various monoclonal antibodies. In this assay, 96 well microtiter dishes (Maxisorp, Nunc, Roskilde, Denmark) were coated overnight with mouse monoclonal antibody (5B6) to gD-1, at a concentration of 2.0 μ g/ml in phosphate buffered saline (PBS). The plates were blocked in a PBS solution containing 0.5% bovine serum albumin (PBSA) and then incubated with growth conditioned cell culture medium from transfected cells expressing the recombinant gp120 variants for 2 hr at room temperature. The plates were washed three times in PBS containing 0.05% Tween 20 and then incubated with the purified, HRPO-conjugated monoclonal antibodies. Following a 1 hr incubation, the plates were washed three times and developed with the colorimetric substrate, o-phenylenediamine (Sigma, St. Louis, Mo.).

The optical densities in each well were then read in a microtiter plate reading spectrophotometer at 492 nm. Each cell culture supernatant containing fragments or mutated rgp120s was normalized for expression based on the titering of its reactivity to the V3 binding monoclonal antibody 1034 or to a rabbit polyclonal antisera to MN-rgp120. Data from these experiments were expressed as a ratio of the optical densities obtained with the CD4 blocking monoclonal antibodies binding to the fragments or MN-rgp120 mutants compared with the full length wild type rgp120s.

To normalize for different concentrations of MN-rgp120-derived protein in the cell culture supernatants, the binding of the CD4 blocking monoclonal antibodies to each preparation was compared to that of an HRPO-conjugated monoclonal antibody to the V3 domain of MN-rgp120 (1034).

Data from these experiments were expressed as a ratio of the optical densities obtained with the CD4 blocking monoclonal antibodies to the HRPO conjugated V3 reactive monoclonal antibody.

CD4 Binding Assays

The ability of monoclonal antibodies to inhibit the binding of MN-rgp120 to recombinant soluble CD4 (rsCD4) was determined in a solid phase radioimmunoassay similar to that described previously (33). The effect of single amino acid substitutions on the binding of MN-rgp120 mutants to CD4 was determined in a co-immunoprecipitation assay similar to that described previously (21). Briefly, 293 cells were metabolically labeled with ^{35}S -methionine 24 hr after transfection with plasmids expressing MN-rgp120 variants. Growth conditioned cell culture medium (0.5 ml) was then incubated with 5.0 μg of recombinant sCD4 for 90 minutes at room temperature. Following this incubation, 5.0 μg of an anti-CD4 monoclonal antibody (465), known to bind to an epitope remote from the gp120 binding site, was added and allowed to incubate another 90 minutes at room temperature.

The gp120-CD4-antibody complexes were precipitated with Pansorbin that had been washed with PBS, preabsorbed with 0.1% bovine serum albumin and then bound with 50 μg of an affinity purified rabbit anti-mouse IgG (Cappel, West Chester, Pa.). The pellet was washed twice with PBS 1% NP-40, 0.05% SDS, and then boiled in beta mercaptoethanol containing SDS-PAGE sample buffer. The immunoprecipitation products were resolved by SDS PAGE and visualized by autoradiography as described previously (1, 21).

Antibody Affinity Measurements

Anti-gp120 antibodies were iodinated with $\text{Na } ^{125}\text{I}$ with iodogen. (Pierce, Rockford, Ill.). Briefly, 50 μg of antibody in PBS was placed in 1.5 ml polypropylene microcentrifuge tubes coated with 50 μg of Iodogen. Two millicuries of carrier free $\text{Na}[^{125}\text{I}]$ was added. After 15 min., free ^{125}I was separated from the labeled protein by chromatography on a PD-10 column (Pierce, Rockford, Ill.) pre-equilibrated in PBS containing 0.5% gelatin. Antibody concentrations following iodination were determined by ELISA to calculate specific activities.

For binding assays, 96-well microtiter plates were coated with 100 μl /well of a 10 $\mu\text{g}/\text{ml}$ solution of MN-rgp120 or IIIBrgp120 in 0.1 M bicarbonate buffer, pH 9.6 and incubated for 2 hr at room temperature or overnight at 4° C. To prevent non-specific binding, plates were blocked for 1–2 hr at room temperature with 200 μl /well of a gelatin solution consisting of PBS containing 0.5% (wt/vol) gelatin and 0.02% sodium azide. Unlabeled anti-gp120 monoclonal antibody (0 to 400 nM) was titrated (in duplicate) in situ and radiolabeled antibody was added to each well at a concentration of 0.5 nM.

After a 1–2 hr incubation at room temperature, the plate was washed 10 \times with the PBS/0.5% gelatin/0.02% azide buffer to remove free antibody. The antibody-gp120 complexes were solubilized with 0.1 N NaOH/0.1% SDS solution and counted in a gamma counter. The data were analyzed by the method of Scatchard (40) using the Ligand analytical software program (31). K_d values reported represent the means of four independent determinations.

RESULTS

Characterization of Monoclonal Antibodies to MN-rgp120 that Block CD4 Binding

Monoclonal antibodies prepared from mice immunized with MN-rgp120 (3, 33), were screened for the ability to bind to MN-rgp120 coated microtiter dishes by ELISA as described previously (33). Of the thirty five clones obtained, seven were identified (1024, 1093, 1096, 1097, 1110, 1112,

and 1127) that were able to inhibit the binding of MN-rgp120 to recombinant CD4 in ELISA (FIG. 1) or solid phase or cell surface radioimmunoassays (21, 33). Previous studies have shown that two distinct classes of CD4 blocking monoclonal antibodies occur: those that bind to conformation dependent (discontinuous) epitopes (16, 26, 33, 35, 45) and those that bind to conformation independent (sequential) epitopes (4, 7, 21, 33, 43).

To distinguish between these two alternatives, the binding of the monoclonal antibodies to denatured (reduced and carboxymethylated) MN-rgp120 (RCM-gp120) was measured by ELISA as described previously (33). As illustrated in Table 4, below, it was found that all of the CD4 blocking monoclonal antibodies reacted with the chemically denatured protein; indicating that they all recognized conformation independent (sequential) epitopes.

TABLE 4

MAb	Properties of monoclonal antibodies to MN-rgp120					rg120 cross reactivity
	CD4 Inhibitors	HIV-1 mn Neutralization	HIV-1 mn V3	CM-rgp120	C4 Domain peptides	
1024	+	+	-	+	-	2
1093	+	+	-	+	-	2
1096	+	+	-	+	-	2
1097	+	+	-	+	-	2
1110	+	+	-	+	-	2
1112	+	+	-	+	-	2
1127	+	+	-	+	-	2
1026	-	+	+	+	-	1, 2, 3, 4, 6
1092	-	-	-	+	-	1, 2, 3, 4, 5
1126	-	-	-	+	-	1, 2, 3, 5, 7
1086	-	-	-	+	-	2
13H8	+	-	-	+	1, 3	1, 2, 3, 4, 5, 6, 7

rgp120 cross reactivity: 1, IIIB-rgp120; 2, MN-rgp120; 3, NYS-rgp120; 4, JrCSF-rgp120; 5, Z6-rgp120; 6, Z321-rgp120; 7, A244-rgp120
C4 domain peptides:
1, FINMWQEVGKAMYAPPIS (SEQ. ID. NO. 24);
2, MWQEVGKAMYAP (SEQ. ID. NO. 25);
3, GKAMYAPPIKQIR (SEQ. ID. NO. 26)

The cross reactivity of these monoclonal antibodies was assessed by ELISA as described previously (33). In these experiments, the ability of the monoclonal antibodies to bind to a panel of seven rgp120s, prepared from the IIIB, MN, Z6, Z321, NY-5, A244, and JRCSF isolates of HIV-1, was measured by ELISA (33). It was found that all of the CD4 blocking monoclonal antibodies were strain specific and bound only to gp120 from the MN strain of HIV-1 (Table 4). However, other antibodies from the same fusion (1026, 1092, and 1126) exhibited much broader cross reactivity (Table 4, FIG. 2), as did a CD4 blocking monoclonal antibody to IIIB-rgp120 (13H8) described previously (33).

Further studies were performed to characterize the neutralizing activity of the antibodies to MN-rgp120. In these studies, monoclonal antibodies were incubated with cell free virus (HIV-1_{MN}), and the resulting mixture was then used to infect MT-2 cells in microtiter plates. After 5 days, the plates were developed by addition of the colorimetric dye, MTT, and cell viability was measured spectrophotometrically. It was found (Table 4, FIG. 2) that all of the CD4 blocking monoclonal antibodies were able to inhibit viral infectivity. However the potency of the monoclonal antibodies varied considerably with some monoclonal antibodies (eg. 1024) able to inhibit infection at very low concentrations (IC_{50} of 0.08 μg per ml) whereas other monoclonal antibodies (eg. 1112) required much higher concentrations (IC_{50} of 30 μg per ml). In control experiments two monoclonal antibodies

to MN-rgp120 from the same fusion (eg.1086, 1092) were ineffective, whereas the 1026 monoclonal antibody exhibited potent neutralizing activity. Similarly, monoclonal antibodies to the V3 domain of IIIB-rgp120 (10F6, 11G5) known to neutralize the infectivity HIV-1_{IIIB} (33), were unable to neutralize the HIV-1_{MN} virus.

Binding studies using synthetic peptides were then performed to further localize the epitopes recognized by these monoclonal antibodies as described previously (33). When a peptide corresponding to the V3 domain (3) of MN-rgp120 was tested, it was found that none of the CD4 blocking antibodies showed any reactivity. However the epitope recognized by the non-CD4 blocking monoclonal antibody, 1026, prepared against MN-rgp120 could be localized to the V3 domain by virtue of its binding to this peptide. In other experiments, three synthetic peptides from the C4 domain of gp120 that incorporated sequences recognized by the CD4 blocking, weakly neutralizing monoclonal antibodies described by McKeating et al. (26) were tested (Table 4). It was found that none of the CD4 blocking monoclonal antibodies to MN-rgp120 reacted with these peptides, however the non-neutralizing, CD4 blocking 13H8 monoclonal antibody bound to the peptides corresponding to residues 423–440 of IIIB-gp120 and residues 431–441 of MN-gp120, but not to that corresponding to residues 426–437 of IIIB-gp120. Thus the 13H8 monoclonal antibody recognized an epitope that was similar, if not identical, to that described by McKeating et al. (26). This result is consistent with the observation that the 13H8 monoclonal antibody and the monoclonal antibodies described by Cordell et al. (4) and McKeating et al. (26) exhibited considerable cross reactivity, whereas the antibodies to MN-rgp120 were highly strain specific.

CD4 Blocking Antibodies Recognize Epitopes in the C4 Domain

Previously, a strain specific, CD4 blocking monoclonal antibody (5C2) raised against IIIB-rgp120 was found to recognize an epitope in the C4 domain of IIIB-rgp120 (21, 33). Although the 5C2 monoclonal antibody was able to block the binding of rgp120 to CD4, it was unable to neutralize HIV-1 infectivity in vitro (7). Affinity columns prepared from 5C2 adsorbed an 11 amino acid peptide (residues 422 to 432) from a tryptic digest of gp120 (21), however monoclonal antibody 5C2 was unable to recognize this peptide coated onto wells of microtiter dishes in an ELISA format (Nakamura et al., unpublished results).

To determine whether the CD4 blocking monoclonal antibodies raised against MN-rgp120 recognized the corresponding epitope in the C4 domain of MN-rgp120, a series of overlapping fragments, spanning the V4 and C4 domains of HIV-1_{MN} gp120, were prepared for expression in mammalian cells. A diagram of the fragments expressed is shown in FIGS. 3A and 3B. The C4 domain fragments were expressed as fusion proteins that incorporated the signal sequence and amino terminal 25 amino acids of HSV-1 glycoprotein D as described above.

Plasmids directing the expression of the chimeric C4 domain fragments were transfected into 293 cells, and their expression was monitored by radioimmunoprecipitation studies where a monoclonal antibody, 5B6, specific for the mature amino terminus of glycoprotein D was utilized. It was found (FIG. 3B) that all of the fragments were expressed and exhibited mobilities on SDS-PAGE gels appropriate for their size. Thus fMN.368–408 (lane 1) exhibited a mobility of 19 kD; fMN.368–451 (lane 2) exhibited a mobility of 29 kD; fMN.419–433 (lane 3) exhibited a mobility of 6 kD, and fMN.414–451 (lane 4) exhibited a mobility of 6.1 kD.

The binding of monoclonal antibody 1024 to the recombinant fragments was then determined by ELISA (as described in Example 1). It was found (FIG. 3A) that monoclonal antibody 1024 reacted with the fragments that contained the entire C4 domain of MN-rgp120 (fMN₃₆₈₋₄₅₁, fMN₄₀₄₋₄₅₅), but failed to bind to a fragment derived from the adjacent V4 domain (fMN₃₆₈₋₄₀₈) or to another fragment that contained V4 domain sequences and the amino terminal half of the C4 domain (fMN₃₆₈₋₄₂₈). The fact that 1024 bound to the fMN₄₁₄₋₄₅₁ and fMN₄₁₉₋₄₄₃ fragments demonstrated that the epitopes recognized by all of these monoclonal antibodies were contained entirely between residues 419 and 443 in the C4 domain.

Residues Recognized by Monoclonal Antibodies that Block Binding of MN-rgp120 to CD4

To identify specific amino acid residues that might be part of the epitopes recognized by these monoclonal antibodies, the sequence of the C4 domain of MN-rgp120 was compared to those of the gp120s from the six other rgp120s that failed to react with the CD4 blocking monoclonal antibodies (FIG. 4). It was noted that the sequence of MN-rgp120 was unique in that K occurred at position 429 whereas the other rgp120s possessed either E, G, or R at this position. Another difference was noted at position 440 where E replaced K or S. To evaluate the significance of these substitutions, a series of point mutations were introduced into the MN-rgp120 gene (FIG. 5). Plasmids expressing the mutant proteins were transfected into 293s cells, and expression was verified by radioimmunoprecipitation with a monoclonal antibody (1034) directed to the V3 domain of MN-rgp120. Cell culture supernatants were harvested and used for the monoclonal antibody binding studies shown in Table 6. To verify expression, radio-immunoprecipitation studies using cell culture supernatants from cells metabolically labeled with [³⁵S]-methionine were performed using the 1024 monoclonal antibody specific for the C4 domain of MN-rgp120 (A) or the 1034 monoclonal antibody specific for the V3 domain of MN-rgp120. Immune complexes were precipitated with the use of fixed *S. aureus* and the adsorbed proteins were resolved by SDS-PAGE. Proteins were visualized by autoradiography. The samples were: Lane 1, MN.419A; lane 2 MN.421A; lane 3 MN.429E; lane 4, MN.429A; lane 5, MN.432A; lane 6, MN.440A; lane 7, MN-rgp120. The immunoprecipitation study showed that 1024 antibody binds well to all the variants except 3 and 4 which are mutated at residue 429. 1034 antibody was used as a control and precipitates with anti-V3 antibodies.

The effect of these mutations on the binding of the CD4 blocking monoclonal antibodies was then evaluated by ELISA as illustrated in Table 5, below.

TABLE 5

Proteins/ MAbs	Binding of CD4 blocking monoclonal antibodies to C4 domain mutants							
	1024	1093	1096	1097	1110	1112	1127	5C2
MN-rgp120	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.05
MN-419A	1.11	1.10	0.94	1.21	0.78	0.95	1.10	ND
MN-421A	1.11	1.60	0.88	1.42	1.34	0.91	1.10	ND
MN-429E	0.03	0.07	0.11	0.04	0.10	0.10	0.02	ND
MN-429A	0.10	0.07	0.14	0.04	0.09	0.11	0.05	ND
MN-432A	0.77	0.15	0.59	0.08	0.12	0.24	0.26	ND
MN-440A	1.06	1.13	1.08	0.87	1.12	1.0	1.3	ND
IIIB-rgp120	0.03	ND	ND	ND	ND	ND	ND	1.0

TABLE 5-continued

Proteins/ MAbs	Binding of CD4 blocking monoclonal antibodies to C4 domain mutants							
	1024	1093	1096	1097	1110	1112	1127	5C2
MN-423F	ND	ND	ND	ND	ND	ND	ND	0.45
MN-423F, 429E	ND	ND	ND	ND	ND	ND	ND	1.09

Data represent the relative binding of MAbs to the native and mutant forms of rgp120. Values were calculated by dividing the binding (determined by ELISA) of the CD4 blocking MAbs to the proteins indicated by the values obtained for the binding of a V3 specific MAb (1034) to the same proteins (as described in Example 1).

It was found that replacement of K₄₄₀ with an A residue (MN.440A) had no effect on the binding of the 1024 monoclonal antibody or any of the other CD4 blocking monoclonal antibodies (Table 5). The significance of K at position 429 was then evaluated by substitution of either A (MN.429A) or E (MN.429E) at this location. It was found that the A for K substitution at position 429 (MN.420A) markedly reduced the binding of the 1024 monoclonal antibody and all of the other CD4 blocking monoclonal antibodies (Table 5). Similarly, the replacement of E for K (MN.429E) at this position totally abrogated the binding of the 1024 monoclonal antibody and all of the other CD4 blocking monoclonal antibodies (Table 5). Several other mutants were constructed to evaluate the role of positively charged residues in the C4 domain. It was found that A for K substitutions at positions 419 (MN.419A) and 421 (MN.421A) failed to interfere with the binding of any of the CD4 blocking monoclonal antibodies as illustrated in Table 6, below.

TABLE 6

MAb	Block	Correlation Between Antibody Binding Affinity and Virus Neutralizing Activity	
		K _d , nM ^c	IC ₅₀ , nM ^d
1024 ^e	+	2.7 ± 0.9	0.4
1086 ^{e,f}	-	9.7 ± 2.2	—
1093 ^e	+	9.9 ± 2.6	3.3
1096 ^c	+	10 ± 6	12
1097 ^e	+	13.4 ± 3.7	12
1110 ^c	+	12.1 ± 1.7	12
1112 ^e	+	20 ± 4.4	200
1127 ^c	+	9.3 ± 4	3.3
1086 ^{e,f}	-	9.7 ± 2.2	—
13H8 ^{f,g}	+ ^b	22 ± 6	—

^aBlocked binding of rgp120 MN to CD4.

^bBlocked binding of rgp120 IIIb, not rgp120 MN, to CD4.

^cMean of four determinations calculated using the method of Scatchard (40).

^dNeutralization of HIV-1_{MN} infectivity in vitro.

^eAnti-rgp120 MN antibody.

^fDid not neutralize HIV-1 infectivity.

^gAnti-rgp120 IIIb antibody.

However, when K at position 432 was replaced with A (MN432.A), the binding of all of the CD4 blocking antibodies was markedly reduced (Table 5). Interestingly, the binding of monoclonal antibody 1024 appeared less affected by this substitution than the other monoclonal antibodies (Table 5). Thus, these studies demonstrated that K₄₂₉ and K₄₃₂ were critical for the binding of all of the CD4 blocking monoclonal antibodies, and that K₄₁₉, K₄₂₁, and K₄₄₀ did not appear to play a role in monoclonal antibody binding. Amino Acids Recognized Monoclonal Antibodies that Block Binding of IIIB-rgp120 to CD4

The identification of residues 429 and 432 as being part of the epitope recognized by the MN-rgp120 specific CD4 blocking monoclonal antibodies was particularly interesting since this region was previously found to be implicated in the binding of the 5C2 monoclonal antibody (21). The properties of the 1024 like-monoclonal antibodies and the 5C2 monoclonal antibody differed from the C4 reactive monoclonal antibodies described by other investigators (4, 43) in that the former appeared strain specific and the latter were broadly cross reactive. To account for the strain specificity of these monoclonal antibodies, the sequence of the eleven amino acid peptide of IIIB-rgp120 recognized by monoclonal antibody 5C2 was compared to the corresponding sequence of MN-rgp120. It was found that the IIIB protein differed from the MNB protein at positions 429 where K replaced E and at position 423 where I replaced F (FIG. 5). Because it was known from previous studies (33) that the 5C2 monoclonal antibody was unable to bind to gp120 from two strains (i.e., NY-5 and JRcsf) that also possessed E at position 423, it seemed unlikely that this position could account for the strain specificity of 5C2. Sequence comparison (FIG. 5) also showed that gp120 from HIV-1_{IIIB} was unique in that a phenylalanine residue occurred at position 423 whereas the other six strains examined possess an I at this position.

To determine whether residues 423 and/or 429 could account for the type specificity of the 5C2 monoclonal antibody, a mutant of MN-rgp120 was constructed which incorporated an F for I replacement at position 423 (MN.423F). In addition, the MN-rgp120 mutant, MN.429E (described above) was further mutagenized to incorporate a F for I substitution at position 423 (MN.423F), thus resulting in a double mutant (MN.423F,429E) whose sequence was identical to that of IIIB-rgp120 within the 10 amino acid 5C2 epitope (FIG. 4). The expression of these mutants in 293s cells was verified by radioimmunoprecipitation using rabbit polyclonal antisera to MN-rgp120. When the binding of the 13H8 monoclonal antibody to a set of mutants incorporating substitutions at position 423 and 429 was examined, it was found that none of the replacements effected the binding of this antibody (data not shown). When the 5C2 monoclonal antibody was examined, it was found that the F for I replacement (MN.423 F) conferred partial reactivity (Table 5). When the double mutant (MN.423F,429E), containing the F for I substitution as well as the E for K substitution was tested, binding that was indistinguishable from that to IIIB-rgp120 was observed (Table 5). These results demonstrated that F at position 423 and E at position 429 both play a role in binding of the 5C2 monoclonal antibody, and suggest that the strain specificity of 5C2 can be attributed to the residues at these positions.

Examination of the sequences of gp120 from the various clones of LAI that have been analyzed revealed that several substrains of LAI differed from each other in the C4 domain. Thus the sequences of the IIIB (30), Bru (46), and HXB3 (6) clones of LAI were identical at positions 423 and 429 where F and E residues occurred respectively. However, the sequence of the HXB2 substrain (36) differed from the others at these positions where, like MN-rgp120, K replaced E and at position 423 where I replaced F (FIG. 5). Similarly, the HX10 and BH10 substrains (36, 37) differed only at position 423 where, like HIV-1_{MN}, I replaced F. Based on the mutagenesis experiments above, it would be predicted that monoclonal antibody 1024 should be able to bind to gp120 from the HXB2 substrain of LAI, but not the HXB3 substrain. If I₄₂₃ was important for binding, then 1024 should also bind the HX10 substrain.

To test this hypothesis, the binding of monoclonal antibody 1024 to the surface cells infected with either IIIB, HXB2, HXB3, and HX10 substrains of HIV-1_{LAI} was measured by flow cytometry. It was found that monoclonal antibody 1024 was able to bind only HXB2 providing further confirmation that residues 423 and 429 were important for the binding of this antibody. The fact that monoclonal antibody 1024 did not bind to HX10 infected cells suggested that I₄₂₃ was not important for the binding of this monoclonal antibody. Thus these studies demonstrate that reactivity with the 1024 monoclonal antibody segregates with the occurrence of F and E residues at positions 423 and 429, respectively, and shows that substrains of HIV-1_{LAI} differ from one another at a functionally significant epitope in the C4 domain.

Neutralizing Activity of CD4 Blocking Antibodies Correlates with their Binding Affinity

To account for the difference in virus neutralizing activity between the CD4 blocking monoclonal antibodies, their gp120 binding affinities were determined by competitive binding of [¹²⁵I]-labeled monoclonal antibody to rgp120 (Table 6). Typical Scatchard these assay data from these assays is shown in FIGS. 7(A to C). Linear, one-site binding kinetics were observed for all the monoclonal antibodies to MN-rgp120, suggesting that only a single class of sites was recognized, and that there was no cooperativity between two combining sites of each immunoglobulin molecule. It was found (FIG. 7A, Table 6) that monoclonal antibody 1024, which exhibited the most potent virus neutralizing activity (IC₅₀ of 0.08 μg per ml), possessed the lowest K_d (2.7 nM). In contrast (FIG. 7C, Table 6), monoclonal antibody 1112, the antibody that exhibited the weakest virus neutralizing activity (IC₅₀ of 30 μg per ml) possessed the highest K_d (20 nM). K_ds for six additional CD4-blocking monoclonal antibodies raised against MN-rgp120 were also determined (Table 6). It was found that monoclonal antibodies that possessed intermediate K_ds similarly possessed intermediate neutralization IC₅₀ values. To explore the relationship between virus neutralizing activity and gp120 binding affinity, the data in Table 6 was plotted in several different ways. It was found that when the K_d of the monoclonal antibodies was plotted as a function of the log of the IC₅₀, a linear relationship was obtained (FIG. 8). Using this analysis a correlation coefficient (r) of 0.97) was obtained. Thus, this graph demonstrates that the virus neutralizing activity of these monoclonal antibodies is directly proportional to the gp120 binding affinity, and that the threshold for neutralization at this epitope is defined by the slope of the graph in FIG. 8.

A similar analysis was performed with the non-neutralizing CD4 blocking monoclonal antibodies to IIIB-rgp120, 5C2 and 13H8. The binding curve for 13H8 (FIG. 7C) showed that it bound to a single class of sites on IIIB-rgp120 with a K_d of 22 nM. The affinity of 5C2 could not be determined by this assay because at antibody concentrations greater than 5 nM, non-linear (reduced gp120 binding) was observed. This effect was suggestive steric hindrance at these concentrations or negative cooperativity between combining sites. The binding affinity was also determined for the non-neutralizing, non-CD4 blocking monoclonal antibody to MN-rgp120, 1086. The fact that this antibody exhibited a binding affinity similar (9.7 nM) to many of the neutralizing monoclonal antibodies but failed to inhibit infectivity, proves that high antibody binding affinity alone is not sufficient for neutralization.

Effect of C4 Domain Mutants on CD4 Binding

Finally, the CD4 binding properties of the series of MN-rgp120 mutants, constructed to localize the C4 domain

epitopes, were measured in a qualitative co-immunoprecipitation assay. In these studies the ability of the mutagenized MN-rgp120 variants to co-immunoprecipitate CD4 was evaluated as described previously (21) in a qualitative co-immunoprecipitation assay similar to that described previously (19). Briefly, 293 cells, transfected with plasmids directing the expression of MN-rgp120 variants described in FIG. 5, were metabolically labeled with [³⁵S]-methionine, and the growth conditioned cell culture supernatants were incubated with rsCD4. The resulting rsCD4:gp120 complexes were then immunoprecipitated by addition of the CD4 specific monoclonal antibody, 465 (A) or a positive control monoclonal antibody (1034) directed to the V3 domain of MN-rgp120 (B). The immunoprecipitated proteins were resolved by SDS-PAGE and visualized by autoradiography as described previously (3). The samples were: Lane 1, MN.419A; lane 2, MN.421A; lane 3, MN.429E; lane 4, MN.429A; lane 5, MN.432A; lane 6, MN.440A; lane 7, MN-rgp120. The gel showed that the mutants that block antibody binding do not block binding of CD4. Therefore, the antibodies do not bind to the gp120 CD4-binding contact residues. This indicates that steric hinderance may inhibit antibody binding, rather than that the antibodies bind directly to the CD4 contact residues to inhibit binding.

It was found that all of the variants in which apolar A residue was substituted for the charged K or E residues (e.g., MN.419A, MN.421A, MN.432A, and MN.440A) were still able to co-immunoprecipitate rsCD4. Similarly, the replacement of E for K at position 429 (MN.429E), the replacement of F for I at position 423 (MN.423F) or the mutant which incorporated both mutation (MN.423F,429E) also showed no reduction in their ability to co-immunoprecipitate rsCD4. Thus, radical amino acid substitutions at five positions failed to affect the binding of gp120 to CD4. These results were consistent with previous studies (5, 21, 34) where it was found that only a few of the many mutations that have been induced in this region effected CD4 binding.

This study indicates that neutralizing epitopes in the C4 domain have now been found to be located between about residues 420 and 440. In addition, the critical residues for antibody binding are residues 429 and 432.

EXAMPLE 2

Identification of V2 Neutralizing Epitopes

The procedures described in Example 1 were used to map epitopes in the V2 region of gp120. Table 7 illustrates the results of mutagenicity studies to map V2 neutralizing epitopes. In the table, the columns indicate the comparison of binding of the monoclonal antibodies with wild type (WT) gp120 in comparison to various mutations of gp120 using standard notation. For example, "G171R" indicates that the glycine (G) at residue 171 has been replaced by an arginine (R). "172A/173A" indicates that the residues at 172 and 173 have been replaced by alanine. The neutralizing monoclonal antibodies tested (MAbs) are listed in the rows. The numerical values in the table are the optical density value of an ELISA assay performed as described in Example 1 to measure the amount of antibody binding. The underlined values indicate significantly reduced binding, indicating the substituted residue is critical for binding of the antibody.

TABLE 7

MAbs	WT	G171R, M174V	172A/ 173A	E187V	187V/ 188S
6E10	1.00	<u>0.10</u>	1.28	0.60	<u>0.25</u>
1017	1.00	0.70	1.10	0.87	<u>0.04</u>
1022	1.00	0.80	1.10	1.00	<u>0.00</u>
1028	1.00	0.90	1.18	1.07	<u>0.04</u>
1029	1.00	0.83	1.16	1.01	<u>0.16</u>
1019	1.00	<u>0.13</u>	1.30	0.75	0.74
1027	1.00	<u>0.00</u>	1.20	0.80	0.64
1025	1.00	0.69	<u>0.00</u>	<u>0.00</u>	0.83
1088	1.00	0.73	1.12	0.94	<u>0.03</u>
13H8	1.00	0.77	0.78	0.48	<u>0.65</u>

MAbs	WT	177A	172A/ 173A	188A	183A
6E10	1.00	<u>0.36</u>	0.52	0.64	0.43
1017	1.00	0.77	0.77	0.76	<u>0.11</u>
1022	1.00	0.86	0.72	<u>0.14</u>	<u>0.00</u>
1028	1.00	0.93	0.78	0.49	<u>0.04</u>
1029	1.00	0.88	0.85	0.53	<u>0.16</u>
1019	1.00	<u>0.16</u>	<u>0.00</u>	0.41	0.44
1027	1.00	<u>0.00</u>	<u>0.02</u>	0.41	0.49
1025	1.00	0.75	0.0	0.83	0.72
1088	1.00	0.77	0.77	0.53	<u>0.00</u>
13H8	1.00	0.72	0.72	0.53	0.60

As illustrated in Table 7, the study demonstrated that there are a series of overlapping neutralizing epitopes from been found to be located in the V2 region (residues 163 through 200), with most of the epitopes located between residues 163 and 200. In addition, the study indicates that the critical residues in the V2 domain for antibody binding are residues 171, 173, 174, 177, 181, 183, 187, and 188.

EXAMPLE 3

Immunization Studies

gp120 from the MN, GNE₈, and GNE₁₆ strains of HIV was prepared by amplifying the gene from each isolate and cloning and expressing the gene in CHO cells as described in Berman et al., *J. Virol.* 66:4464–4469 (1992). Briefly, the gp160 gene was amplified with two rounds of amplification using the following nested primers according to the protocol by Kellog et al., pp 337–347 in *PCR Protocols: a guide to methods and amplification*. Innis et al. (eds.) Academic Press, Inc., New York.

First round primers:

AATAATAGCAATAGTTGTGTGGWCC (W is A or T)
ATTCCTTCCCTTAYAGTAGGCCATCC (Y is T or C)

Second round primers:

GGGAATTCGGATCCAGAGCAGAAGA-CAGTGGCAATGA

GTCAAGAATTCTTATAGCAAAGCCCTTCCAA

The primers are SEQ. ID. NOs. 31–34. Each gene is then digested with the restriction endonucleases KpnI and AccI. The resulting fragment was subcloned into the Bluescript (+) phagemid M13 vector (Stratagene, Inc.) and sequenced by the dideoxynucleotide method (Sanger et al., *Proc. Natl. Acad. Sci. USA* 74:5463–5467 (1977)).

A fragment of the gp120 coding region was then used to construct a chimeric gene for expression in mammalian cells, as described in Lasky et al., *Science* 223:209–212 (1986). The 5' end was fused to a polylinker adjacent to a simian virus 40 (SV40) promoter and the 3' end was fused to a polylinker adjacent to the 3' untranslated sequences containing an SV40 polyadenylation signal. The expression vector (MN-rgp120) was co-transfected in CHO cells defi-

cient in production of the enzyme dihydrofolate reductase, along with a plasmid (pSVdhfr) containing a cDNA encoding the selectable marker, dihydrofolate reductase. Cell lines expressing MN-rgp120 were isolated as described in Lasky et al., *Science* 223:209–212 (1986). The recombinant glycoprotein was purified from growth-conditioned cell culture medium by immunoaffinity and ion exchange chromatography as described in Leonard et al., *J. Biol. Chem.* 265:10373–10382 (1990).

gp120 from the GNE₈ and GNE₁₆ strains of HIV is prepared in the same manner as described for the MN isolate.

MN-rgp120 (300 μ g/injection), GNE₈-rgp120 (300 μ g/injection), and GNE₁₆-rgp120 (300 μ g/injection) are prepared in an aluminum hydroxide adjuvant (as described in Cordonnier et al., *Nature* 340:571–574 (1989)). Six chimpanzees are injected at 0, 4, and 32 weeks. Sera are collected and assayed for neutralizing antibody to each strain of HIV at the time of each immunization and three weeks thereafter. At 35 weeks, each of the chimpanzees has significant levels of neutralizing antibodies to each strain.

At 35 weeks, the chimpanzees are randomly assigned to three groups. Each group is challenged with about 10 50% chimpanzee-infectious doses (CID₅₀) each of one of the vaccine isolates. One unimmunized chimpanzee (control) is also injected with the same amount of virus as the immunized chimpanzees for each vaccine strain.

Sera are drawn every two weeks throughout the study and assayed for antibodies to HIV core proteins and for the presence of HIV by PCR amplification and co-cultivation of peripheral blood mononuclear cells (PBMCs) from the chimpanzee together with activated human or chimpanzee PBMCs. The presence of antibodies to core proteins indicates the presence of viral infection as does the detection of amplified viral DNA or viral infection of co-cultivated cells.

The presence of virus is detected by PCR and co-cultivation methods in each unimmunized control animal between weeks 2 and 4 post challenge. Antibodies to core proteins appear in the control chimpanzees at six weeks post challenge. Neither virus nor antibodies are at detectable levels in any of the immunized chimpanzees at one year post challenge, indicating that the vaccine effectively protects the chimpanzees from infection from each of the challenge strains.

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 SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 33

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
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His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
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Gln Glu Val Glu Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp Lys
 85 90 95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
 100 105 110

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 115 120 125

Asn Cys Thr Asp Leu Arg Asn Thr Thr Asn Thr Asn Asn Ser Thr Asp
 130 135 140

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 145 150 155 160

Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Gly Asp Lys Met Gln Lys
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 180 185 190

Ser Thr Ser Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln
 195 200 205

Ala Cys Pro Lys Ile Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
 210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Ser Gly
 225 230 235 240

Lys Gly Ser Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
 245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
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 275 280 285

Ile Ile Val His Leu Lys Glu Ser Val Gln Ile Asn Cys Thr Arg Pro

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Ile	Ser	Arg	Ala	Lys	Trp	Asn	Asp	Thr	Leu	Arg	Gln	Ile	Val	Ser	Lys
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Leu	Lys	Glu	Gln	Phe	Lys	Asn	Lys	Thr	Ile	Val	Phe	Asn	Pro	Ser	Ser
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Gly	Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu
		370					375					380			
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Asn	Asn	Thr	Trp	Asn	Asn	Thr	Thr	Gly	Ser	Asn	Asn	Asn	Ile	Thr	Leu
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Gln	Cys	Lys	Ile	Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Lys	Val	Gly	Lys
			420					425					430		
Ala	Met	Tyr	Ala	Pro	Pro	Ile	Glu	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn
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Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Glu	Asp	Thr	Asp	Thr
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Asn	Asp	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn
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Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Thr	Ile	Glu	Pro	Leu
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys	Tyr	Ala	Leu	Ala	Asp	Ala	Ser	Leu	Lys	Met	Ala	Asp	Pro	Asn	Arg
1				5					10					15	
Phe	Arg	Gly	Lys	Asp	Leu	Pro	Val	Leu	Asp	Gln	Leu	Leu	Glu	Val	Pro
			20					25					30		
Val	Trp	Lys	Glu	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys
		35					40						45		
Ala	Tyr	Asp	Thr	Glu	Ala	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val
		50				55					60				
Pro	Thr	Asp	Pro	Asn	Pro	Gln	Glu	Val	Glu	Leu	Val	Asn	Val	Thr	Glu
65					70					75				80	
Asn	Phe	Asn	Met	Trp	Lys	Asn	Asn	Met	Val	Glu	Gln	Met	His	Glu	Asp
				85					90					95	
Ile	Ile	Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr
			100					105					110		
Pro	Leu	Cys	Val	Thr	Leu	Asn	Cys	Thr	Asp	Leu	Arg	Asn	Thr	Thr	Asn
		115					120					125			
Thr	Asn	Asn	Ser	Thr	Asp	Asn	Asn	Asn	Ser	Lys	Ser	Glu	Gly	Thr	Ile
						135						140			

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Lys	Gly	Gly	Glu	Met	Lys	Asn	Cys	Ser	Phe	Asn	Ile	Thr	Thr	Ser	Ile
145					150					155					160
Gly	Asp	Lys	Met	Gln	Lys	Glu	Tyr	Ala	Leu	Leu	Tyr	Lys	Leu	Asp	Ile
				165					170					175	
Glu	Pro	Ile	Asp	Asn	Asp	Ser	Thr	Ser	Tyr	Arg	Leu	Ile	Ser	Cys	Asn
			180					185					190		
Thr	Ser	Val	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Ile	Ser	Phe	Glu	Pro	Ile
		195					200					205			
Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys	Cys	Asn
	210					215					220				
Asp	Lys	Lys	Phe	Ser	Gly	Lys	Gly	Ser	Cys	Lys	Asn	Val	Ser	Thr	Val
225					230					235					240
Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu
				245					250					255	
Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Glu	Asp	Phe
			260					265					270		
Thr	Asp	Asn	Ala	Lys	Thr	Ile	Ile	Val	His	Leu	Lys	Glu	Ser	Val	Gln
		275					280					285			
Ile	Asn	Cys	Thr	Arg	Pro	Asn	Tyr	Asn	Lys	Arg	Lys	Arg	Ile	His	Ile
	290					295					300				
Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Lys	Asn	Ile	Lys	Gly	Thr	Ile
305					310					315					320
Arg	Gln	Ala	His	Cys	Ile	Ile	Ser	Arg	Ala	Lys	Trp	Asn	Asp	Thr	Leu
				325					330					335	
Arg	Gln	Ile	Val	Ser	Lys	Leu	Lys	Glu	Gln	Phe	Lys	Asn	Lys	Thr	Ile
			340					345					350		
Val	Phe	Asn	Pro	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser
		355					360					365			
Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Ser	Pro	Leu	Phe
	370					375					380				
Asn	Ser	Ile	Trp	Asn	Gly	Asn	Asn	Thr	Trp	Asn	Asn	Thr	Thr	Gly	Ser
385					390					395					400
Asn	Asn	Asn	Ile	Thr	Leu	Gln	Cys	Lys	Ile	Lys	Gln	Ile	Ile	Asn	Met
			405						410					415	
Trp	Gln	Lys	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Glu	Gly	Gln
			420					425					430		
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly
		435					440					445			
Gly	Glu	Asp	Thr	Asp	Thr	Asn	Asp	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly
	450					455					460				
Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val
465					470					475					480
Val	Thr	Ile	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	Ala	Lys	Arg	Arg
				485					490					495	
Val	Val	Gln	Arg	Glu											
				500											

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala
 1 5 10 15

Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys Arg Ile Lys Gln Phe Ile Asn Met Trp Gln Glu Val Gly Lys Ala
 1 5 10 15

Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala
 1 5 10 15

Met Tyr Ala Pro Pro Ile Lys Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Gly Val Gly Lys Ala
 1 5 10 15

Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Asn Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly Lys Ala
 1 5 10 15

Ile Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:

-continued

- (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Arg Ile Lys Gln Ile Val Asn Met Trp Gln Arg Val Gly Gln Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Lys Gly Val Ile Lys Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Gly Ala Gly Gln Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Ser Gly Thr Ile Asn Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Arg Ile Lys Gln Phe Ile Asn Met Trp Gln Glu Val Gly Lys Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys

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20

25

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly
 1 5 10 15
 Glu Phe Phe Tyr Cys Asn Thr Ser Pro Leu Phe Asn Ser Ile Trp Asn
 20 25 30
 Gly Asn Asn Thr Trp Asn Asn Thr Thr Gly Ser Asn Asn Asn Ile Thr
 35 40 45
 Leu Gln Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly
 50 55 60
 Lys Ala Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys Ser Ser
 65 70 75 80
 Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
 85 90

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Ala Val Gly Lys Ala
 1 5 10 15

-continued

Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Cys Ala Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala
 1 5 10 15

Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Cys Lys Ile Ala Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala
 1 5 10 15

Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Ala Ala
 1 5 10 15

Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Cys Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala
 1 5 10 15

Met Tyr Ala Pro Pro Ile Ala Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

-continued

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Arg Ile Lys Gln Phe Ile Asn Met Trp Gln Glu Val Gly Lys Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Lys Ile Lys Gln Phe Ile Asn Met Trp Gln Lys Val Gly Lys Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Lys Ile Lys Gln Phe Ile Asn Met Trp Gln Glu Val Gly Lys Ala
 1 5 10 15
 Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Phe Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro
 1 5 10 15
 Ile Ser

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Lys Ala Met Tyr Ala Pro Pro Ile Lys Gly Gln Ile Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2552 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG ATA GTG AAG GGG ATC AGG AAG AAT TGT CAG CAC TTG TGG AGA TGG	48
Met Ile Val Lys Gly Ile Arg Lys Asn Cys Gln His Leu Trp Arg Trp	
1 5 10 15	
GGC ACC ATG CTC CTT GGG ATG TTG ATG ATC TGT AGT GCT GCA GAA AAA	96
Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Lys	
20 25 30	
TTG TGG GTC ACA GTC TAT TAT GGG GTA CCT GTG TGG AAA GAA GCA ACC	144
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr	
35 40 45	
ACC ACT CTA TTT TGT GCA TCA GAT GCT AAA GCA TAT GAT ACA GAG GTA	192
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val	
50 55 60	
CAT AAT GTT TGG GCC ACA CAT GCC TGT GTA CCC ACA GAC CCC AAC CCA	240
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro	
65 70 75 80	
CAA GAA ATA GGA TTG GAA AAT GTA ACA GAA AAT TTT AAC ATG TGG AAA	288
Gln Glu Ile Gly Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys	
85 90 95	
AAT AAC ATG GTA GAA CAG ATG CAT GAG GAT ATA ATC AGT TTA TGG GAT	336
Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp	
100 105 110	
CAA AGC TTA AAG CCA TGT GTA AAA TTA ACC CCA CTA TGT GTT ACT TTA	384
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu	
115 120 125	
AAT TGC ACT GAT TTG AAA AAT GCT ACT AAT ACC ACT AGT AGC AGC TGG	432
Asn Cys Thr Asp Leu Lys Asn Ala Thr Asn Thr Thr Ser Ser Ser Trp	
130 135 140	
GGA AAG ATG GAG AGA GGA GAA ATA AAA AAC TGC TCT TTC AAT GTC ACC	480
Gly Lys Met Glu Arg Gly Glu Ile Lys Asn Cys Ser Phe Asn Val Thr	
145 150 155 160	
ACA AGT ATA AGA GAT AAG ATG AAG AAT GAA TAT GCA CTT TTT TAT AAA	528
Thr Ser Ile Arg Asp Lys Met Lys Asn Glu Tyr Ala Leu Phe Tyr Lys	
165 170 175	
CTT GAT GTA GTA CCA ATA GAT AAT GAT AAT ACT AGC TAT AGG TTG ATA	576
Leu Asp Val Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr Arg Leu Ile	
180 185 190	
AGT TGT AAC ACC TCA GTC ATT ACA CAG GCC TGT CCA AAG GTG TCC TTT	624
Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe	
195 200 205	
GAG CCA ATT CCC ATA CAT TAT TGT GCC CCG GCT GGT TTT GCG ATT CTA	672
Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu	

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210	215	220	
AAG TGT AGA GAT AAA AAG TTC AAC GGA ACA GGA CCA TGT ACA AAT GTC Lys Cys Arg Asp Lys Lys Phe Asn Gly Thr Gly Pro Cys Thr Asn Val 225 230 235 240			720
AGC ACA GTA CAA TGT ACA CAT GGA ATT AGG CCA GTA GTA TCA ACT CAA Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln 245 250 255			768
CTG CTG TTA AAT GGC AGT TTA GCA GAA GAA GAA GTA GTA ATT AGA TCT Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser 260 265 270			816
GCC AAT TTC TCG GAC AAT GCT AAA ACC ATA ATA GTA CAG CTG AAC GAA Ala Asn Phe Ser Asp Asn Ala Lys Thr Ile Ile Val Gln Leu Asn Glu 275 280 285			864
TCT GTA GAA ATT AAT TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser 290 295 300			912
ATA CAT ATA GGA CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile 305 310 315 320			960
GGA GAC ATA AGA CAA GCA CAT TGT AAC CTT AGT AGC ACA AAA TGG AAT Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Ser Thr Lys Trp Asn 325 330 335			1008
AAT ACT TTA AAA CAG ATA GTT ACA AAA TTA AGA GAA CAT TTT AAT AAA Asn Thr Leu Lys Gln Ile Val Thr Lys Leu Arg Glu His Phe Asn Lys 340 345 350			1056
ACA ATA GTC TTT AAT CAC TCC TCA GGA GGG GAC CCA GAA ATT GTA ATG Thr Ile Val Phe Asn His Ser Ser Gly Gly Asp Pro Glu Ile Val Met 355 360 365			1104
CAC AGT TTT AAT TGT GGA GGG GAA TTT TTC TAC TGT AAT ACA ACA CCA His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Thr Thr Pro 370 375 380			1152
CTG TTT AAT AGT ACT TGG AAT TAT ACT TAT ACT TGG AAT AAT ACT GAA Leu Phe Asn Ser Thr Trp Asn Tyr Thr Tyr Thr Trp Asn Asn Thr Glu 385 390 395 400			1200
GGG TCA AAT GAC ACT GGA AGA AAT ATC ACA CTC CAA TGC AGA ATA AAA Gly Ser Asn Asp Thr Gly Arg Asn Ile Thr Leu Gln Cys Arg Ile Lys 405 410 415			1248
CAA ATT ATA AAC ATG TGG CAG GAA GTA GGA AAA GCA ATG TAT GCC CCT Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro 420 425 430			1296
CCC ATA AGA GGA CAA ATT AGA TGC TCA TCA AAT ATT ACA GGG CTG CTA Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu 435 440 445			1344
TTA ACA AGA GAT GGT GGT AAT AAC AGC GAA ACC GAG ATC TTC AGA CCT Leu Thr Arg Asp Gly Gly Asn Asn Ser Glu Thr Glu Ile Phe Arg Pro 450 455 460			1392
GGA GGA GGA GAT ATG AGG GAC AAT TGG AGA AGT GAA TTA TAT AAA TAT Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr 465 470 475 480			1440
AAA GTA GTA AAA ATT GAA CCA TTA GGA GTA GCA CCC ACC AAG GCA AAG Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys 485 490 495			1488
AGA AGA GTG ATG CAG AGA GAA AAA AGA GCA GTG GGA ATA GGA GCT GTG Arg Arg Val Met Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val 500 505 510			1536
TTC CTT GGG TTC TTG GGA GCA GCA GGA AGC ACT ATG GGC GCA GCG TCA Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser 515 520 525			1584
GTG ACG CTG ACG GTA CAG GCC AGA CTA TTA TTG TCT GGT ATA GTG CAA			1632

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Val	Thr	Leu	Thr	Val	Gln	Ala	Arg	Leu	Leu	Leu	Ser	Gly	Ile	Val	Gln	
	530					535					540					
CAG	CAG	AAC	AAT	TTG	CTG	AGG	GCT	ATT	GAG	GCC	GAA	CAG	CAT	CTG	TTG	1680
Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Glu	Gln	His	Leu	Leu	
545					550					555					560	
CAA	CTC	ACA	GTC	TGG	GGC	ATC	AAG	CAG	CTC	CAG	GCA	AGA	GTC	CTG	GCT	1728
Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Ala	Arg	Val	Leu	Ala	
				565					570					575		
GTG	GAG	AGA	TAC	CTA	AAG	GAT	CAA	CAG	CTC	CTG	GGG	ATT	TGG	GGT	TGC	1776
Val	Glu	Arg	Tyr	Leu	Lys	Asp	Gln	Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys	
			580					585					590			
TCT	GGA	AAA	CTC	ATC	TGC	ACC	ACT	GCT	GTG	CCT	TGG	AAT	GCT	AGT	TGG	1824
Ser	Gly	Lys	Leu	Ile	Cys	Thr	Thr	Ala	Val	Pro	Trp	Asn	Ala	Ser	Trp	
		595					600						605			
AGT	AAT	AAA	TCT	CTG	GAT	AAG	ATT	TGG	GAT	AAC	ATG	ACC	TGG	ATG	GAG	1872
Ser	Asn	Lys	Ser	Leu	Asp	Lys	Ile	Trp	Asp	Asn	Met	Thr	Trp	Met	Glu	
	610					615					620					
TGG	GAA	AGA	GAA	ATT	GAC	AAT	TAC	ACA	AGC	TTA	ATA	TAC	AGC	TTA	ATT	1920
Trp	Glu	Arg	Glu	Ile	Asp	Asn	Tyr	Thr	Ser	Leu	Ile	Tyr	Ser	Leu	Ile	
625					630					635					640	
GAA	GAA	TCG	CAG	AAC	CAA	CAA	GAA	AAA	AAT	GAA	CAA	GAA	TTA	TTG	GAA	1968
Glu	Glu	Ser	Gln	Asn	Gln	Glu	Lys	Asn	Glu	Gln	Glu	Glu	Leu	Leu	Glu	
				645				650						655		
TTA	GAT	AAA	TGG	GCA	AGT	TTG	TGG	AAT	TGG	TTT	GAC	ATA	ACA	AAA	TGG	2016
Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn	Trp	Phe	Asp	Ile	Thr	Lys	Trp	
			660					665					670			
CTG	TGG	TAT	ATA	AAA	ATA	TTC	ATA	ATG	ATA	GTA	GGA	GGC	TTG	GTA	GGT	2064
Leu	Trp	Tyr	Ile	Lys	Ile	Phe	Ile	Met	Ile	Val	Gly	Gly	Leu	Val	Gly	
		675				680						685				
TTA	AGA	ATA	GTT	TTT	ACT	GTA	CTT	TCT	ATA	GTG	AAT	AGA	GTT	AGG	AAG	2112
Leu	Arg	Ile	Val	Phe	Thr	Val	Leu	Ser	Ile	Val	Asn	Arg	Val	Arg	Lys	
	690					695					700					
GGA	TAC	TCA	CCA	TTA	TCG	TTC	CAG	ACC	CAC	CTC	CCA	GCC	CCG	AGG	GGA	2160
Gly	Tyr	Ser	Pro	Leu	Ser	Phe	Gln	Thr	His	Leu	Pro	Ala	Pro	Arg	Gly	
705					710					715					720	
CTC	GAC	AGG	CCC	GAA	GGA	ACC	GAA	GAA	GAA	GGT	GGA	GAG	CGA	GAC	AGA	2208
Leu	Asp	Arg	Pro	Glu	Gly	Thr	Glu	Glu	Glu	Gly	Gly	Glu	Arg	Asp	Arg	
				725						730				735		
GAC	AGA	TCC	AGT	CGA	TTA	GTG	GAT	GGA	TTC	TTA	GCA	ATT	GTC	TGG	GTC	2256
Asp	Arg	Ser	Ser	Arg	Leu	Val	Asp	Gly	Phe	Leu	Ala	Ile	Val	Trp	Val	
			740					745					750			
GAC	CTG	CGG	AGC	CTG	TGC	CTC	TTC	AGC	TAC	CAC	CGC	TTG	AGA	GAC	TTA	2304
Asp	Leu	Arg	Ser	Leu	Cys	Leu	Phe	Ser	Tyr	His	Arg	Leu	Arg	Asp	Leu	
		755				760						765				
CTC	TTG	ATT	GCA	GCG	AGG	ATT	GTG	GAA	CTT	CTG	GGA	CGC	AGG	GGG	TGG	2352
Leu	Leu	Ile	Ala	Ala	Arg	Ile	Val	Glu	Leu	Leu	Gly	Arg	Arg	Gly	Trp	
	770					775					780					
GAA	GCC	CTC	AAA	TAT	TGG	TGG	AAT	CTC	CTA	CAG	TAT	TGG	ATT	CAG	GAA	2400
Glu	Ala	Leu	Lys	Tyr	Trp	Trp	Asn	Leu	Leu	Gln	Tyr	Trp	Ile	Gln	Glu	
785					790					795					800	
CTA	AAG	AAT	AGT	GCT	GTT	AGC	TTG	CTC	AAT	GCC	ACA	GCC	ATA	GCA	GTA	2448
Leu	Lys	Asn	Ser	Ala	Val	Ser	Leu	Leu	Asn	Ala	Thr	Ala	Ile	Ala	Val	
				805						810				815		
GCT	GAG	GGA	ACA	GAT	AGG	GTT	ATA	GAA	ATA	GTA	CAA	AGA	GCT	TAT	AGA	2496
Ala	Glu	Gly	Thr	Asp	Arg	Val	Ile	Glu	Ile	Val	Gln	Arg	Ala	Tyr	Arg	
			820					825					830			
GCT	ATT	CTC	CAC	ATA	CCC	ACA	CGA	ATA	AGA	CAG	GGC	TTG	GAA	AGG	GCT	2544
Ala	Ile	Leu	His	Ile	Pro	Thr	Arg	Ile	Arg	Gln	Gly	Leu	Glu	Arg	Ala	
		835					840						845			

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TTG CTA TA
Leu Leu
850

2552

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ile Val Lys Gly Ile Arg Lys Asn Cys Gln His Leu Trp Arg Trp
1 5 10 15

Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Lys
20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Ile Gly Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
85 90 95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Asn Cys Thr Asp Leu Lys Asn Ala Thr Asn Thr Thr Ser Ser Ser Trp
130 135 140

Gly Lys Met Glu Arg Gly Glu Ile Lys Asn Cys Ser Phe Asn Val Thr
145 150 155 160

Thr Ser Ile Arg Asp Lys Met Lys Asn Glu Tyr Ala Leu Phe Tyr Lys
165 170 175

Leu Asp Val Val Pro Ile Asp Asn Asp Asn Thr Ser Tyr Arg Leu Ile
180 185 190

Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe
195 200 205

Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu
210 215 220

Lys Cys Arg Asp Lys Lys Phe Asn Gly Thr Gly Pro Cys Thr Asn Val
225 230 235 240

Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln
245 250 255

Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser
260 265 270

Ala Asn Phe Ser Asp Asn Ala Lys Thr Ile Ile Val Gln Leu Asn Glu
275 280 285

Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser
290 295 300

Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile
305 310 315 320

Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Ser Thr Lys Trp Asn
325 330 335

Asn Thr Leu Lys Gln Ile Val Thr Lys Leu Arg Glu His Phe Asn Lys

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Thr	Ile	Val	Phe	Asn	His	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Met
		355					360					365			
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Thr	Pro
	370				375						380				
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Tyr	Thr	Tyr	Thr	Trp	Asn	Asn	Thr	Glu
385					390					395					400
Gly	Ser	Asn	Asp	Thr	Gly	Arg	Asn	Ile	Thr	Leu	Gln	Cys	Arg	Ile	Lys
				405					410					415	
Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro
			420					425					430		
Pro	Ile	Arg	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu
		435					440					445			
Leu	Thr	Arg	Asp	Gly	Gly	Asn	Asn	Ser	Glu	Thr	Glu	Ile	Phe	Arg	Pro
	450					455					460				
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
465					470					475					480
Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	Ala	Lys
				485					490					495	
Arg	Arg	Val	Met	Gln	Arg	Glu	Lys	Arg	Ala	Val	Gly	Ile	Gly	Ala	Val
			500					505					510		
Phe	Leu	Gly	Phe	Leu	Gly	Ala	Ala	Gly	Ser	Thr	Met	Gly	Ala	Ala	Ser
		515					520					525			
Val	Thr	Leu	Thr	Val	Gln	Ala	Arg	Leu	Leu	Leu	Ser	Gly	Ile	Val	Gln
	530					535						540			
Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Glu	Gln	His	Leu	Leu
545					550					555					560
Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Ala	Arg	Val	Leu	Ala
				565					570					575	
Val	Glu	Arg	Tyr	Leu	Lys	Asp	Gln	Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys
			580					585					590		
Ser	Gly	Lys	Leu	Ile	Cys	Thr	Thr	Ala	Val	Pro	Trp	Asn	Ala	Ser	Trp
		595					600						605		
Ser	Asn	Lys	Ser	Leu	Asp	Lys	Ile	Trp	Asp	Asn	Met	Thr	Trp	Met	Glu
	610					615					620				
Trp	Glu	Arg	Glu	Ile	Asp	Asn	Tyr	Thr	Ser	Leu	Ile	Tyr	Ser	Leu	Ile
625					630					635					640
Glu	Glu	Ser	Gln	Asn	Gln	Gln	Glu	Lys	Asn	Glu	Gln	Glu	Leu	Leu	Glu
				645					650					655	
Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn	Trp	Phe	Asp	Ile	Thr	Lys	Trp
			660					665					670		
Leu	Trp	Tyr	Ile	Lys	Ile	Phe	Ile	Met	Ile	Val	Gly	Gly	Leu	Val	Gly
		675					680					685			
Leu	Arg	Ile	Val	Phe	Thr	Val	Leu	Ser	Ile	Val	Asn	Arg	Val	Arg	Lys
	690					695					700				
Gly	Tyr	Ser	Pro	Leu	Ser	Phe	Gln	Thr	His	Leu	Pro	Ala	Pro	Arg	Gly
705					710					715					720
Leu	Asp	Arg	Pro	Glu	Gly	Thr	Glu	Glu	Glu	Gly	Gly	Glu	Arg	Asp	Arg
				725					730					735	
Asp	Arg	Ser	Ser	Arg	Leu	Val	Asp	Gly	Phe	Leu	Ala	Ile	Val	Trp	Val
			740					745					750		
Asp	Leu	Arg	Ser	Leu	Cys	Leu	Phe	Ser	Tyr	His	Arg	Leu	Arg	Asp	Leu
	755						760						765		

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Leu Leu Ile Ala Ala Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp
 770 775 780

Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ile Gln Glu
 785 790 795 800

Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val
 805 810 815

Ala Glu Gly Thr Asp Arg Val Ile Glu Ile Val Gln Arg Ala Tyr Arg
 820 825 830

Ala Ile Leu His Ile Pro Thr Arg Ile Arg Gln Gly Leu Glu Arg Ala
 835 840 845

Leu Leu
 850

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATG AGA GTG AAG GGG ATC AGG AGG AAT TAT CAG CAC TTG TGG AGA TGG	48
Met Arg Val Lys Gly Ile Arg Arg Asn Tyr Gln His Leu Trp Arg Trp	
1 5 10 15	
GGC ACC ATG CTC CTT GGG ATA TTG ATG ATC TGT AGT GCT GCA GGG AAA	96
Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Ala Gly Lys	
20 25 30	
TTG TGG GTC ACA GTC TAT TAT GGG GTA CCT GTG TGG AAA GAA ACA ACC	144
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Thr Thr	
35 40 45	
ACC ACT CTA TTT TGT GCA TCA GAT GCT AAA GCA TAT GAT ACA GAG ATA	192
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ile	
50 55 60	
CAT AAT GTT TGG GCC ACA CAT GCC TGT GTA CCC ACA GAC CCC AAC CCA	240
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro	
65 70 75 80	
CAA GAA GTA GTA TTG GAA AAT GTG ACA GAA AAT TTT AAC ATG TGG AAA	288
Gln Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys	
85 90 95	
AAT AAC ATG GTG GAA CAG ATG CAT GAG GAT ATA ATC AGT TTA TGG GAT	336
Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp	
100 105 110	
CAA AGT TTA AAG CCA TGT GTA AAA TTA ACC CCA CTC TGT GTT ACT TTA	384
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu	
115 120 125	
AAT TGC ACT GAT GCG GGG AAT ACT ACT AAT ACC AAT AGT AGT AGC AGG	432
Asn Cys Thr Asp Ala Gly Asn Thr Thr Asn Thr Asn Ser Ser Ser Arg	
130 135 140	
GAA AAG CTG GAG AAA GGA GAA ATA AAA AAC TGC TCT TTC AAT ATC ACC	480
Glu Lys Leu Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn Ile Thr	
145 150 155 160	
ACA AGC GTG AGA GAT AAG ATG CAG AAA GAA ACT GCA CTT TTT AAT AAA	528
Thr Ser Val Arg Asp Lys Met Gln Lys Glu Thr Ala Leu Phe Asn Lys	
165 170 175	

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CTT	GAT	ATA	GTA	CCA	ATA	GAT	GAT	GAT	GAT	AGG	AAT	AGT	ACT	AGG	AAT	576
Leu	Asp	Ile	Val	Pro	Ile	Asp	Asp	Asp	Asp	Arg	Asn	Ser	Thr	Arg	Asn	
			180					185					190			
AGT	ACT	AAC	TAT	AGG	TTG	ATA	AGT	TGT	AAC	ACC	TCA	GTC	ATT	ACA	CAG	624
Ser	Thr	Asn	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	
		195					200					205				
GCC	TGT	CCA	AAG	GTA	TCA	TTT	GAG	CCA	ATT	CCC	ATA	CAT	TTC	TGT	ACC	672
Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Phe	Cys	Thr	
		210				215					220					
CCG	GCT	GGT	TTT	GCG	CTT	CTA	AAG	TGT	AAT	AAT	AAG	ACG	TTC	AAT	GGA	720
Pro	Ala	Gly	Phe	Ala	Leu	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	
		225			230					235					240	
TCA	GGA	CCA	TGC	AAA	AAT	GTC	AGC	ACA	GTA	CAA	TGT	ACA	CAT	GGA	ATT	768
Ser	Gly	Pro	Cys	Lys	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	
				245					250					255		
AGG	CCA	GTA	GTA	TCA	ACT	CAA	CTG	CTG	TTA	AAT	GGC	AGT	CTA	GCA	GAA	816
Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	
			260				265						270			
GGA	GAG	GTA	GTA	ATT	AGA	TCT	GAA	AAT	TTC	ACG	AAC	AAT	GCT	AAA	ACC	864
Gly	Glu	Val	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asn	Asn	Ala	Lys	Thr	
		275					280					285				
ATA	ATA	GTA	CAG	CTG	ACA	GAA	CCA	GTA	AAA	ATT	AAT	TGT	ACA	AGA	CCC	912
Ile	Ile	Val	Gln	Leu	Thr	Glu	Pro	Val	Lys	Ile	Asn	Cys	Thr	Arg	Pro	
		290				295					300					
AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CCT	ATA	GGA	CCA	GGG	AGA	GCA	TTT	960
Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Pro	Ile	Gly	Pro	Gly	Arg	Ala	Phe	
		305			310					315					320	
TAT	GCA	ACA	GGA	GAC	ATA	ATA	GGA	AAT	ATA	AGA	CAA	GCA	CAT	TGT	AAC	1008
Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asn	Ile	Arg	Gln	Ala	His	Cys	Asn	
				325					330					335		
CTT	AGT	AGA	ACA	GAC	TGG	AAT	AAC	ACT	TTA	GGA	CAG	ATA	GTT	GAA	AAA	1056
Leu	Ser	Arg	Thr	Asp	Trp	Asn	Asn	Thr	Leu	Gly	Gln	Ile	Val	Glu	Lys	
			340					345					350			
TTA	AGA	GAA	CAA	TTT	GGG	AAT	AAA	ACA	ATA	ATC	TTT	AAT	CAC	TCC	TCA	1104
Leu	Arg	Glu	Gln	Phe	Gly	Asn	Lys	Thr	Ile	Ile	Phe	Asn	His	Ser	Ser	
		355				360						365				
GGA	GGG	GAC	CCA	GAA	ATT	GTA	ATG	CAC	AGT	TTT	AAT	TGT	AGA	GGG	GAA	1152
Gly	Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Arg	Gly	Glu	
		370				375					380					
TTT	TTC	TAC	TGT	AAT	ACA	ACA	CAA	TTG	TTT	GAC	AGT	ACT	TGG	GAT	AAT	1200
Phe	Phe	Tyr	Cys	Asn	Thr	Thr	Gln	Leu	Phe	Asp	Ser	Thr	Trp	Asp	Asn	
		385			390					395					400	
ACT	AAA	GTG	TCA	AAT	GGC	ACT	AGC	ACT	GAA	GAG	AAT	AGC	ACA	ATC	ACA	1248
Thr	Lys	Val	Ser	Asn	Gly	Thr	Ser	Thr	Glu	Glu	Asn	Ser	Thr	Ile	Thr	
				405					410					415		
CTC	CCA	TGC	AGA	ATA	AAG	CAA	ATT	GTA	AAC	ATG	TGG	CAG	GAA	GTA	GGA	1296
Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Val	Asn	Met	Trp	Gln	Glu	Val	Gly	
			420					425					430			
AAA	GCA	ATG	TAT	GCC	CCT	CCC	ATC	AGA	GGA	CAA	ATT	AGA	TGT	TCA	TCA	1344
Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Arg	Gly	Gln	Ile	Arg	Cys	Ser	Ser	
		435					440					445				
AAT	ATT	ACA	GGG	TTG	CTA	TTA	ACA	AGA	GAT	GGA	GGT	AGT	AAC	AAC	AGC	1392
Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Ser	Asn	Asn	Ser	
		450				455					460					
ATG	AAT	GAG	ACC	TTC	AGA	CCT	GGA	GGA	GGA	GAT	ATG	AGG	GAC	AAT	TGG	1440
Met	Asn	Glu	Thr	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	
		465			470					475					480	
AGA	AGT	GAA	TTA	TAC	AAA	TAT	AAA	GTA	GTA	AAA	ATT	GAA	CCA	TTA	GGA	1488
Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	

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															485																490																495	
GTA	GCA	CCC	ACC	AAG	GCA	AAG	AGA	AGA	GTG	GTG	CAG	AGA	GAA	AAA	AGA	1536	Val	Ala	Pro	Thr	Lys	Ala	Lys	Arg	Arg	Val	Val	Gln	Arg	Glu	Lys	Arg	500	505	510													
GCA	GTG	GGA	ATA	GGA	GCT	GTG	TTC	CTT	GGG	TTC	TTA	GGA	GCA	GCA	GGA	1584	Ala	Val	Gly	Ile	Gly	Ala	Val	Phe	Leu	Gly	Phe	Leu	Gly	Ala	Ala	Gly	515	520	525													
AGC	ACT	ATG	GGC	GCA	GCG	TCA	ATA	ACG	CTG	ACG	GTA	CAG	GCC	AGA	CTA	1632	Ser	Thr	Met	Gly	Ala	Ala	Ser	Ile	Thr	Leu	Thr	Val	Gln	Ala	Arg	Leu	530	535	540													
TTA	TTG	TCT	GGT	ATA	GTG	CAA	CAG	CAG	AAC	AAT	TTG	CTG	AGG	GCT	ATT	1680	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	545	550	555	560												
GAG	GCG	CAA	CAG	CAT	CTG	TTG	CAA	CTC	ATA	GTC	TGG	GGC	ATC	AAG	CAG	1728	Glu	Ala	Gln	Gln	His	Leu	Leu	Gln	Leu	Ile	Val	Trp	Gly	Ile	Lys	Gln	565	570	575													
CTC	CAG	GCA	AGA	GTC	CTG	GCT	GTG	GAA	AGA	TAC	CTA	AGG	GAT	CAA	CAG	1776	Leu	Gln	Ala	Arg	Val	Leu	Ala	Val	Glu	Arg	Tyr	Leu	Arg	Asp	Gln	Gln	580	585	590													
CTC	CTG	GGG	ATT	TGG	GGT	TGC	TCT	GGA	AAA	CTC	ATT	TGC	ACC	ACC	TCA	1824	Leu	Leu	Gly	Ile	Trp	Gly	Cys	Ser	Gly	Lys	Leu	Ile	Cys	Thr	Thr	Ser	595	600	605													
GTG	CCT	TGG	AAT	GCT	AGT	TGG	AGT	AAT	AAA	TCT	CTA	GAT	AAG	ATT	TGG	1872	Val	Pro	Trp	Asn	Ala	Ser	Trp	Ser	Asn	Lys	Ser	Leu	Asp	Lys	Ile	Trp	610	615	620													
GAT	AAC	ATG	ACC	TGG	ATG	GAG	TGG	GAA	AGA	GAA	ATT	GAG	AAT	TAC	ACA	1920	Asp	Asn	Met	Thr	Trp	Met	Glu	Trp	Glu	Arg	Glu	Ile	Glu	Asn	Tyr	Thr	625	630	635	640												
AGC	TTA	ATA	TAC	ACC	TTA	ATT	GAA	GAA	TCG	CAG	AAC	CAA	CAA	GAA	AAG	1968	Ser	Leu	Ile	Tyr	Thr	Leu	Ile	Glu	Glu	Ser	Gln	Asn	Gln	Gln	Glu	Lys	645	650	655													
AAT	GAA	CAA	GAC	TTA	TTG	GAA	TTG	GAT	CAA	TGG	GCA	AGT	CTG	TGG	AAT	2016	Asn	Glu	Gln	Asp	Leu	Leu	Glu	Leu	Asp	Gln	Trp	Ala	Ser	Leu	Trp	Asn	660	665	670													
TGG	TTT	AGC	ATA	ACA	AAA	TGG	CTG	TGG	TAT	ATA	AAA	ATA	TTC	ATA	ATG	2064	Trp	Phe	Ser	Ile	Thr	Lys	Trp	Leu	Trp	Tyr	Ile	Lys	Ile	Phe	Ile	Met	675	680	685													
ATA	GTT	GGA	GGC	TTG	GTA	GGT	TTA	AGA	ATA	GTT	TTT	GCT	GTA	CTT	TCT	2112	Ile	Val	Gly	Gly	Leu	Val	Gly	Leu	Arg	Ile	Val	Phe	Ala	Val	Leu	Ser	690	695	700													
ATA	GTG	AAT	AGA	GTT	AGG	CAG	GGA	TAC	TCA	CCA	TTA	TCG	TTT	CAG	ACC	2160	Ile	Val	Asn	Arg	Val	Arg	Gln	Gly	Tyr	Ser	Pro	Leu	Ser	Phe	Gln	Thr	705	710	715	720												
CGC	CTC	CCA	GCC	CCG	AGG	AGA	CCC	GAC	AGG	CCC	GAA	GGA	ATC	GAA	GAA	2208	Arg	Leu	Pro	Ala	Pro	Arg	Arg	Pro	Asp	Arg	Pro	Glu	Gly	Ile	Glu	Glu	725	730	735													
GAA	GGT	GGA	GAG	CAA	GGC	AGA	GAC	AGA	TCC	ATT	CGC	TTA	GTG	GAT	GGA	2256	Glu	Gly	Gly	Glu	Gln	Gly	Arg	Asp	Arg	Ser	Ile	Arg	Leu	Val	Asp	Gly	740	745	750													
TTC	TTA	GCA	CTT	ATC	TGG	GAC	GAC	CTA	CGG	AGC	CTG	TGC	CTC	TTC	AGC	2304	Phe	Leu	Ala	Leu	Ile	Trp	Asp	Asp	Leu	Arg	Ser	Leu	Cys	Leu	Phe	Ser	755	760	765													
TAC	CAC	CGC	TTG	AGA	GAC	TTA	CTC	TTG	ATT	GCA	ACG	AGG	ATT	GTG	GAA	2352	Tyr	His	Arg	Leu	Arg	Asp	Leu	Leu	Leu	Ile	Ala	Thr	Arg	Ile	Val	Glu	770	775	780													
CTT	CTG	GGA	CGC	AGG	GGG	TGG	GAA	GCC	CTC	AAA	TAT	TGG	TGG	AAT	CTC	2400	Leu	Leu	Gly	Arg	Arg	Gly	Trp	Glu	Ala	Leu	Lys	Tyr	Trp	Trp	Asn	Leu	785	790	795	800												
CTA	CAG	TAT	TGG	ATT	CAG	GAA	CTA	AAG	AAT	AGT	GCT	GTT	AGC	TTG	CTT	2448																																

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Leu	Gln	Tyr	Trp	Ile	Gln	Glu	Leu	Lys	Asn	Ser	Ala	Val	Ser	Leu	Leu	
				805					810					815		
AAT	GTC	ACA	GCC	ATA	GCA	GTA	GCT	GAG	GGG	ACA	GAT	AGG	GTT	TTA	GAA	2496
Asn	Val	Thr	Ala	Ile	Ala	Val	Ala	Glu	Gly	Thr	Asp	Arg	Val	Leu	Glu	
			820					825					830			
GTA	TTA	CAA	AGA	GCT	TAT	AGA	GCT	ATT	CTC	CAC	ATA	CCT	ACA	AGA	ATA	2544
Val	Leu	Gln	Arg	Ala	Tyr	Arg	Ala	Ile	Leu	His	Ile	Pro	Thr	Arg	Ile	
		835					840					845				
AGA	CAG	GGC	TTG	GAA	AGG	GCT	TTG	CTA	TA							2573
Arg	Gln	Gly	Leu	Glu	Arg	Ala	Leu	Leu								
	850					855										

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Arg	Val	Lys	Gly	Ile	Arg	Arg	Asn	Tyr	Gln	His	Leu	Trp	Arg	Trp	
1				5					10					15		
Gly	Thr	Met	Leu	Leu	Gly	Ile	Leu	Met	Ile	Cys	Ser	Ala	Ala	Gly	Lys	
			20					25					30			
Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu	Thr	Thr	
		35					40					45				
Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Thr	Glu	Ile	
		50				55					60					
His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	Asn	Pro	
65					70					75					80	
Gln	Glu	Val	Val	Leu	Glu	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met	Trp	Lys	
				85					90					95		
Asn	Asn	Met	Val	Glu	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	Trp	Asp	
			100					105					110			
Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr	Leu	
		115					120					125				
Asn	Cys	Thr	Asp	Ala	Gly	Asn	Thr	Thr	Asn	Thr	Asn	Ser	Ser	Ser	Arg	
		130				135						140				
Glu	Lys	Leu	Glu	Lys	Gly	Glu	Ile	Lys	Asn	Cys	Ser	Phe	Asn	Ile	Thr	
145					150					155					160	
Thr	Ser	Val	Arg	Asp	Lys	Met	Gln	Lys	Glu	Thr	Ala	Leu	Phe	Asn	Lys	
				165					170					175		
Leu	Asp	Ile	Val	Pro	Ile	Asp	Asp	Asp	Asp	Arg	Asn	Ser	Thr	Arg	Asn	
			180					185						190		
Ser	Thr	Asn	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	
		195					200					205				
Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Phe	Cys	Thr	
		210				215						220				
Pro	Ala	Gly	Phe	Ala	Leu	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	
225					230					235					240	
Ser	Gly	Pro	Cys	Lys	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	
				245						250				255		
Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	
			260					265					270			
Gly	Glu	Val	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asn	Asn	Ala	Lys	Thr	
		275					280						285			

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Ile Ile Val Gln Leu Thr Glu Pro Val Lys Ile Asn Cys Thr Arg Pro
 290 295 300
 Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly Pro Gly Arg Ala Phe
 305 310 315 320
 Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile Arg Gln Ala His Cys Asn
 325 330 335
 Leu Ser Arg Thr Asp Trp Asn Asn Thr Leu Gly Gln Ile Val Glu Lys
 340 345 350
 Leu Arg Glu Gln Phe Gly Asn Lys Thr Ile Ile Phe Asn His Ser Ser
 355 360 365
 Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Arg Gly Glu
 370 375 380
 Phe Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asp Ser Thr Trp Asp Asn
 385 390 395 400
 Thr Lys Val Ser Asn Gly Thr Ser Thr Glu Glu Asn Ser Thr Ile Thr
 405 410 415
 Leu Pro Cys Arg Ile Lys Gln Ile Val Asn Met Trp Gln Glu Val Gly
 420 425 430
 Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
 435 440 445
 Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Ser Asn Asn Ser
 450 455 460
 Met Asn Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp
 465 470 475 480
 Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly
 485 490 495
 Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg
 500 505 510
 Ala Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly
 515 520 525
 Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Leu
 530 535 540
 Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile
 545 550 555 560
 Glu Ala Gln Gln His Leu Leu Gln Leu Ile Val Trp Gly Ile Lys Gln
 565 570 575
 Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Arg Asp Gln Gln
 580 585 590
 Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ser
 595 600 605
 Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Asp Lys Ile Trp
 610 615 620
 Asp Asn Met Thr Trp Met Glu Trp Glu Arg Glu Ile Glu Asn Tyr Thr
 625 630 635 640
 Ser Leu Ile Tyr Thr Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys
 645 650 655
 Asn Glu Gln Asp Leu Leu Glu Leu Asp Gln Trp Ala Ser Leu Trp Asn
 660 665 670
 Trp Phe Ser Ile Thr Lys Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met
 675 680 685
 Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser
 690 695 700

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Ile	Val	Asn	Arg	Val	Arg	Gln	Gly	Tyr	Ser	Pro	Leu	Ser	Phe	Gln	Thr
705					710					715					720
Arg	Leu	Pro	Ala	Pro	Arg	Arg	Pro	Asp	Arg	Pro	Glu	Gly	Ile	Glu	Glu
				725					730					735	
Glu	Gly	Gly	Glu	Gln	Gly	Arg	Asp	Arg	Ser	Ile	Arg	Leu	Val	Asp	Gly
			740					745					750		
Phe	Leu	Ala	Leu	Ile	Trp	Asp	Asp	Leu	Arg	Ser	Leu	Cys	Leu	Phe	Ser
		755					760					765			
Tyr	His	Arg	Leu	Arg	Asp	Leu	Leu	Leu	Ile	Ala	Thr	Arg	Ile	Val	Glu
	770					775					780				
Leu	Leu	Gly	Arg	Arg	Gly	Trp	Glu	Ala	Leu	Lys	Tyr	Trp	Trp	Asn	Leu
785					790					795					800
Leu	Gln	Tyr	Trp	Ile	Gln	Glu	Leu	Lys	Asn	Ser	Ala	Val	Ser	Leu	Leu
				805					810					815	
Asn	Val	Thr	Ala	Ile	Ala	Val	Ala	Glu	Gly	Thr	Asp	Arg	Val	Leu	Glu
			820					825					830		
Val	Leu	Gln	Arg	Ala	Tyr	Arg	Ala	Ile	Leu	His	Ile	Pro	Thr	Arg	Ile
		835					840					845			
Arg	Gln	Gly	Leu	Glu	Arg	Ala	Leu	Leu							
	850					855									

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATG	AGA	GTG	AAG	AGG	ATC	AGG	AGG	AAT	TAT	CAG	CAC	TTG	TGG	AAA	TGG	48
Met	Arg	Val	Lys	Arg	Ile	Arg	Arg	Asn	Tyr	Gln	His	Leu	Trp	Lys	Trp	
1				5					10					15		
GGC	ACC	ATG	CTC	CTT	GGG	ATG	TTG	ATG	ATC	TGT	AGT	GCT	GCA	GGA	AAA	96
Gly	Thr	Met	Leu	Leu	Gly	Met	Leu	Met	Ile	Cys	Ser	Ala	Ala	Gly	Lys	
			20					25					30			
TTG	TGG	GTC	ACA	GTC	TAT	TAT	GGG	GTA	CCT	GTG	TGG	AAA	GAA	ACA	ACC	144
Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu	Thr	Thr	
		35					40					45				
ACC	ACT	CTA	TTT	TGT	GCA	TCA	GAT	GCT	AAA	GCA	TAT	GAT	ACA	GAG	ATA	192
Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Thr	Glu	Ile	
		50				55					60					
CAT	AAT	GTT	TGG	GCC	ACA	CAT	GCC	TGT	GTA	CCC	ACA	GAC	CCC	AAC	CCA	240
His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	Asn	Pro	
65					70					75					80	
CAA	GAA	GTA	GTA	TTG	GAA	AAT	GTG	ACA	GAA	AAT	TTT	AAC	ATG	TGG	AAA	288
Gln	Glu	Val	Val	Leu	Glu	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met	Trp	Lys	
				85					90					95		
AAT	AAC	ATG	GTG	GAA	CAG	ATG	CAT	GAG	GAT	ATA	ATC	AGT	TTA	TGG	GAT	336
Asn	Asn	Met	Val	Glu	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	Trp	Asp	
			100					105					110			
CAA	AGT	CTA	AAG	CCA	TGT	GTA	AAA	TTA	ACC	CCA	CTC	TGT	GTT	ACT	TTA	384
Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr	Leu	
		115					120					125				

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AAT TGC ACT GAT GCG GGG AAT ACT ACT AAT ACC AAT AGT AGT AGC GGG Asn Cys Thr Asp Ala Gly Asn Thr Thr Asn Thr Asn Ser Ser Ser Gly 130 135 140	432
GAA AAG CTG GAG AAA GGA GAA ATA AAA AAC TGC TCT TTC AAT ATC ACC Glu Lys Leu Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn Ile Thr 145 150 155 160	480
ACA AGC ATG AGA GAT AAG ATG CAG AGA GAA ACT GCA CTT TTT AAT AAA Thr Ser Met Arg Asp Lys Met Gln Arg Glu Thr Ala Leu Phe Asn Lys 165 170 175	528
CTT GAT ATA GTA CCA ATA GAT GAT GAT GAT AGG AAT AGT ACT AGG AAT Leu Asp Ile Val Pro Ile Asp Asp Asp Arg Asn Ser Thr Arg Asn 180 185 190	576
AGT ACT AAC TAT AGG TTG ATA AGT TGT AAC ACC TCA GTC ATT ACA CAG Ser Thr Asn Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln 195 200 205	624
GCC TGT CCA AAG GTA TCA TTT GAG CCA ATT CCC ATA CAT TTC TGT ACC Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Thr 210 215 220	672
CCG GCT GGT TTT GCG CTT CTA AAG TGT AAT AAT GAG ACG TTC AAT GGA Pro Ala Gly Phe Ala Leu Leu Lys Cys Asn Asn Glu Thr Phe Asn Gly 225 230 235 240	720
TCA GGA CCA TGC AAA AAT GTC AGC ACA GTA CTA TGT ACA CAT GGA ATT Ser Gly Pro Cys Lys Asn Val Ser Thr Val Leu Cys Thr His Gly Ile 245 250 255	768
AGG CCA GTA GTA TCA ACT CAA CTG CTG TTA AAT GGC AGT CTA GCA GGA Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Gly 260 265 270	816
GAA GAG GTA GTA ATT AGA TCT GAA AAT TTC ACG AAC AAT GCT AAA ACC Glu Glu Val Val Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr 275 280 285	864
ATA ATA GTA CAG CTC AAA GAA CCA GTA AAA ATT AAT TGT ACA AGA CCC Ile Ile Val Gln Leu Lys Glu Pro Val Lys Ile Asn Cys Thr Arg Pro 290 295 300	912
AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA CCA GGG AGA GCA TTT Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly Pro Gly Arg Ala Phe 305 310 315 320	960
TAT GCA ACA GGC GAC ATA ATA GGA AAT ATA AGA CAA GCA CAT TGT AAC Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile Arg Gln Ala His Cys Asn 325 330 335	1008
CTT AGT AGA ACA GAC TGG AAT AAC ACT TTA AGA CAG ATA GCT GAA AAA Leu Ser Arg Thr Asp Trp Asn Asn Thr Leu Arg Gln Ile Ala Glu Lys 340 345 350	1056
TTA AGA AAA CAA TTT GGG AAT AAA ACA ATA ATC TTT AAT CAC TCC TCA Leu Arg Lys Gln Phe Gly Asn Lys Thr Ile Ile Phe Asn His Ser Ser 355 360 365	1104
GGA GGG GAC CCA GAA ATT GTA ATG CAC AGT TTT AAT TGT AGA GGG GAA Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Arg Gly Glu 370 375 380	1152
TTT TTC TAC TGT GAT ACA ACA CAA TTG TTT AAC AGT ACT TGG AAT GCA Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser Thr Trp Asn Ala 385 390 395 400	1200
AAT AAC ACT GAA AGG AAT AGC ACT AAA GAG AAT AGC ACA ATC ACA CTC Asn Asn Thr Glu Arg Asn Ser Thr Lys Glu Asn Ser Thr Ile Thr Leu 405 410 415	1248
CCA TGC AGA ATA AAA CAA ATT GTA AAC ATG TGG CAG GAA GTA GGA AAA Pro Cys Arg Ile Lys Gln Ile Val Asn Met Trp Gln Glu Val Gly Lys 420 425 430	1296
GCA ATG TAT GCC CCT CCC ATC AGA GGA CAA ATT AGA TGT TCA TCA AAT Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn 435 440 445	1344

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755	760	765	
CAC CGC TTG AGA GAC TTA CTC TTG ATT GCA ACG AGG ATT GTG GAA CTT His Arg Leu Arg Asp Leu Leu Leu Ile Ala Thr Arg Ile Val Glu Leu 770 775 780			2352
CTG GGA CGC AGG GGG TGG GAA GCC CTC AAA TAT TGG TGG AAT CTC CTA Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu 785 790 795 800			2400
CAG TAT TGG ATT CAG GAA CTA AAG AAT AGT GCT GTT AGC TTG CTT AAT Gln Tyr Trp Ile Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn 805 810 815			2448
GTC ACA GCC ATA GCA GTA GCT GAG GGG ACA GAT AGG GTT CTA GAA GCA Val Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Leu Glu Ala 820 825 830			2496
TTG CAA AGA GCT TAT AGA GCT ATT CTC CAC ATA CCT ACA AGA ATA AGA Leu Gln Arg Ala Tyr Arg Ala Ile Leu His Ile Pro Thr Arg Ile Arg 835 840 845			2544
CAA GGC TTG GAA AGG GCT TTG CTA TA Gln Gly Leu Glu Arg Ala Leu Leu 850 855			2570

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Arg Val Lys Arg Ile Arg Arg Asn Tyr Gln His Leu Trp Lys Trp 1 5 10 15
Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Gly Lys 20 25 30
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Thr Thr 35 40 45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ile 50 55 60
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro 65 70 75 80
Gln Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys 85 90 95
Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp 100 105 110
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu 115 120 125
Asn Cys Thr Asp Ala Gly Asn Thr Thr Asn Thr Asn Ser Ser Ser Gly 130 135 140
Glu Lys Leu Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn Ile Thr 145 150 155 160
Thr Ser Met Arg Asp Lys Met Gln Arg Glu Thr Ala Leu Phe Asn Lys 165 170 175
Leu Asp Ile Val Pro Ile Asp Asp Asp Arg Asn Ser Thr Arg Asn 180 185 190
Ser Thr Asn Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln 195 200 205
Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Phe Cys Thr 210 215 220

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Pro	Ala	Gly	Phe	Ala	Leu	Leu	Lys	Cys	Asn	Asn	Glu	Thr	Phe	Asn	Gly
225					230					235					240
Ser	Gly	Pro	Cys	Lys	Asn	Val	Ser	Thr	Val	Leu	Cys	Thr	His	Gly	Ile
				245					250					255	
Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Gly
			260					265					270		
Glu	Glu	Val	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asn	Asn	Ala	Lys	Thr
		275					280					285			
Ile	Ile	Val	Gln	Leu	Lys	Glu	Pro	Val	Lys	Ile	Asn	Cys	Thr	Arg	Pro
	290					295					300				
Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Pro	Ile	Gly	Pro	Gly	Arg	Ala	Phe
305					310					315					320
Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asn	Ile	Arg	Gln	Ala	His	Cys	Asn
				325					330					335	
Leu	Ser	Arg	Thr	Asp	Trp	Asn	Asn	Thr	Leu	Arg	Gln	Ile	Ala	Glu	Lys
			340					345					350		
Leu	Arg	Lys	Gln	Phe	Gly	Asn	Lys	Thr	Ile	Ile	Phe	Asn	His	Ser	Ser
		355					360					365			
Gly	Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Arg	Gly	Glu
		370				375					380				
Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Ala
385					390					395					400
Asn	Asn	Thr	Glu	Arg	Asn	Ser	Thr	Lys	Glu	Asn	Ser	Thr	Ile	Thr	Leu
			405						410					415	
Pro	Cys	Arg	Ile	Lys	Gln	Ile	Val	Asn	Met	Trp	Gln	Glu	Val	Gly	Lys
			420					425					430		
Ala	Met	Tyr	Ala	Pro	Pro	Ile	Arg	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn
		435					440					445			
Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Ser	Ser	Asn	Ser	Met
	450					455					460				
Asn	Glu	Thr	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg
465					470					475					480
Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	Val
				485					490					495	
Ala	Pro	Thr	Lys	Ala	Met	Arg	Arg	Val	Val	Gln	Arg	Glu	Lys	Arg	Ala
			500					505					510		
Val	Gly	Ile	Gly	Ala	Val	Phe	Leu	Gly	Phe	Leu	Gly	Ala	Ala	Gly	Ser
		515					520					525			
Thr	Met	Gly	Ala	Ala	Ser	Ile	Thr	Leu	Thr	Val	Gln	Ala	Arg	Leu	Leu
	530					535					540				
Leu	Ser	Gly	Ile	Val	Gln	Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu
545					550					555					560
Ala	Gln	Gln	His	Leu	Leu	Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu
				565					570					575	
Gln	Ala	Arg	Val	Leu	Ala	Val	Glu	Arg	Tyr	Leu	Arg	Asp	Gln	Gln	Leu
			580					585					590		
Leu	Gly	Ile	Trp	Gly	Cys	Ser	Gly	Lys	Leu	Ile	Cys	Thr	Thr	Ser	Val
		595					600					605			
Pro	Trp	Asn	Ala	Ser	Trp	Ser	Asn	Lys	Ser	Leu	Asp	Lys	Ile	Trp	Asp
	610					615					620				
Asn	Met	Thr	Trp	Met	Glu	Trp	Glu	Arg	Glu	Ile	Glu	Asn	Tyr	Thr	Ser
625					630					635					640
Leu	Ile	Tyr	Thr	Leu	Ile	Glu	Glu	Ser	Gln	Asn	Gln	Gln	Glu	Lys	Asn

-continued

645	650	655
Lys Gln Asp Leu Leu Glu Leu Asp Gln		
660	665	
 (2) INFORMATION FOR SEQ ID NO:33:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 190 amino acids		
(B) TYPE: amino acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:		
Ala Ser Leu Trp Asn Trp Phe Ser Ile Thr Lys Trp Leu Trp Tyr Ile		
1	5	10
Lys Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val		
	20	25
Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro		
	35	40
Leu Ser Phe Gln Thr Arg Leu Pro Ala Pro Arg Gly Pro Asp Arg Pro		
	50	55
Lys Gly Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Asp Arg Ser Ile		
65	70	75
Arg Leu Val Asp Gly Phe Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser		
	85	90
Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Ala		
	100	105
Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys		
	115	120
Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ile Gln Glu Leu Lys Asn Ser		
	130	135
Ala Val Ser Leu Leu Asn Val Thr Ala Ile Ala Val Ala Glu Gly Thr		
145	150	155
Asp Arg Val Leu Glu Ala Leu Gln Arg Ala Tyr Arg Ala Ile Leu His		
	165	170
Ile Pro Thr Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Leu		
	180	185
		190

What is claimed is:

1. A polypeptide comprising a truncated gp120 sequence comprising the V2, V3, and C4 domains of gp120, which polypeptide lacks the gp120 C5 domain.

2. The polypeptide of claim 1 wherein the polypeptide lacks the gp120 region extending from the carboxy terminus through amino acid residue 453 of the gp120 V5 domain, as numbered from the N-terminal methionine of gp120 from the MN strain of HIV.

3. The polypeptide of claim 2 wherein the polypeptide lacks the gp120 V5 and C5 domains.

4. The polypeptide of claim 1 wherein the polypeptide additionally lacks the gp120 signal sequence.

5. The polypeptide of claim 4 wherein the polypeptide lacks the gp120 region extending from the amino terminus through amino acid residue 111 of the gp120 C1 domain, as numbered from the N-terminal methionine of gp120 from the MN strain of HIV.

6. The polypeptide of claim 4 wherein the polypeptide lacks the gp120 region extending from the amino terminus through amino acid residue 117 of the gp120 C1 domain, as numbered from the N-terminal methionine of gp120 from the MN strain of HIV.

7. The polypeptide of claim 1 wherein the polypeptide lacks the gp120 regions extending from the amino terminus of gp120 through residue 111 of the C1 domain and from residue 453 through the carboxy terminus of gp120, as numbered from the N-terminal methionine of gp120 from the MN strain of HIV.

8. The truncated gp120 sequence of claim 1 wherein the sequence is produced by recombinant engineering.

9. A polypeptide comprising a truncated gp120 sequence comprising the V2, V3, and C4 domains of gp120, which sequence is from a gp120 polypeptide selected from the group consisting of MN_{GNE}-gp120, GNE₈-gp120, and GNE₁₆-gp120, wherein said polypeptide lacks the gp120 signal sequence.

10. The polypeptide of claim 9, wherein the truncated gp120 sequence is joined to a heterologous signal sequence.

11. The polypeptide of claim 10, wherein the heterologous signal sequence is joined to amino acid residue 41 of said truncated gp120 sequence, as numbered from the N-terminal methionine of gp120 from the MN strain of HIV.

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12. The polypeptide of claim **10**, wherein the heterologous signal sequence is derived from the herpes simplex glycoprotein gD1.

13. The polypeptide of claim **12**, wherein the heterologous signal sequence is joined to amino acid residue 41 of said truncated gp120, as numbered from the N-terminal methionine of gp120 from the MN strain of HIV.

14. The polypeptide of claim **13**, wherein the heterologous signal sequence comprises is joined to amino acid

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residue 41 of said truncated gp120 via a sequence derived from the herpes simplex glycoprotein gD-1 signal sequence.

15. The polypeptide of claim **9**, wherein the truncated gp120 sequence is joined to a heterologous sequence derived from the herpes simplex glycoprotein gD-1.

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